

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:24:46 ; Search time 21 Seconds  
(without alignments)  
59.547 Million cell updates/sec

Title: US-09-761-636A-5

Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1827

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.5	46.5	12	2	PT0216
2	30	41.7	12	2	S47394
3	29.5	41.0	13	2	S47357
4	29	40.3	12	2	S25549
5	28	38.9	12	2	PH1463
6	28	38.9	12	2	PH1466
7	28	38.9	13	2	S47400
8	27	37.5	11	2	PT0217
9	27	37.5	12	2	S47391
10	27	37.5	13	2	S47383
11	26	36.1	11	2	S57575
12	26	36.1	12	2	S47395
13	26	36.1	13	2	S47381
14	25.5	35.4	13	2	S47382
15	25	34.7	10	2	S23371
16	25	34.7	11	2	PH0947
17	25	34.7	12	2	PH1469
18	25	34.7	12	2	PH0931
19	24.5	34.0	12	2	PH1457
20	24	33.3	11	2	PH1583
21	24	33.3	12	2	S26552
22	24	33.3	12	2	S26559
23	24	33.3	12	2	S26554
24	24	33.3	12	2	S47363
25	24	33.3	12	2	PH1467
26	24	33.3	12	2	PH1468
27	24	33.3	13	2	S47390
28	23.5	32.6	12	2	PH1459
29	23.5	32.6	13	2	S47377

30 23 31.9 12 2 S26557 T-cell receptor be  
31 23 31.9 12 2 S26556 T-cell receptor be  
32 23 31.9 12 2 S26553 T-cell receptor be  
33 23 31.9 12 2 PH1462 T-cell receptor be  
34 23 31.9 12 2 PH1470 T-cell receptor be  
35 23 31.9 12 2 PH1464 T-cell receptor be  
36 23 31.9 13 2 A23695 myosin heavy chain  
37 22.5 31.2 12 2 S26541 T-cell receptor be  
38 22.5 31.2 12 2 PH1458 T-cell receptor be  
39 22.5 31.2 13 2 S47356 T-cell antigen rec  
40 22.5 31.2 13 2 S47378 T-cell antigen rec  
41 22.5 31.2 13 2 S47385 T-cell antigen rec  
42 22 30.6 10 2 PH0927 T-cell receptor be  
43 22 30.6 12 2 S26546 T-cell receptor be  
44 22 30.6 12 2 S26547 T-cell receptor be  
45 22 30.6 12 2 S26555 T-cell receptor be

ALIGNMENTS

RESULT 1

PT0216  
T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C:Accession: PT0216  
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrictive

A:Reference number: PT0209; MUID:91217621; PMID:1902501  
A:Accession: PT0216  
A:Molecule type: mRNA  
A:Residues: 1-12 <NAK>  
C:Keywords: T-cell receptor

Query Match 46.5%; Score 33.5; DB 2; Length 12;  
Best Local Similarity 72.7%; Pred. No. 12;  
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11  
||| ||| |||  
DB 1 CASSLG-TTNT 10

RESULT 2

S47394  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47394; S47369  
R:Rehner, P.J.

submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell  
A:Reference number: S47355  
A:Accession: S47394  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <LEH>  
A:Cross-references: EMBL:Z35714; NID:G527523; PIDN:CAA84783.1; PID:G527524; EMBL:Z35694;

Query Match 41.7%; Score 30; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 51;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 12  
||| ||| |||  
DB 1 CASSIGNGYTTF 12

RESULT 3

S47357

T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47357  
R:Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell receptor VJ junction beta chain (clone A24/10.1) - mouse (fragment)  
A:Reference number: S47355  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>  
A:Cross-references: EMBL:Z356681; NID:g527451; PIDN:CAA84750.1; PID:g527452  
C:Keywords: T-cell receptor

Query Match 41.0%; Score 29.5; DB 2; Length 13;  
Best Local Similarity 63.6%; Pred. No. 68;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;  
QY 1 CASELGKSTNT 11  
||| |::|  
Db 1 CASS-GRSTDT 10  
||| |::|

RESULT 4  
S26549  
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C:Accession: S26549; S26550  
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: S26549  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Cross-references: EMBL:X67999  
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8  
A:Accession: S26550  
A:Molecule type: mRNA  
A:Residues: 1-12 <CA2>  
A:Cross-references: EMBL:X68000  
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1  
A:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: T-cell receptor

Query Match 40.3%; Score 29; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 77;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CASELGKS 8  
||| |::|  
Db 1 CASSLGST 8  
||| |::|

RESULT 5  
PH1463  
T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1463  
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1463  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CASELGKS 8  
||| |::|  
Db 1 CASSLGNT 8  
||| |::|

RESULT 6  
PH1466  
T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1466  
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1466  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 38.9%; Score 28; DB 2; Length 12;  
Best Local Similarity 71.4%; Pred. No. 1.2e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CASELGK 7  
||| |::|  
Db 1 CASSLGQ 7  
||| |::|

RESULT 7  
S47400  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47400  
R:Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A:Reference number: S47355  
A:Accession: S47400  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>  
A:Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536  
C:Keywords: T-cell receptor

Query Match 38.9%; Score 28; DB 2; Length 13;  
Best Local Similarity 41.7%; Pred. No. 1.3e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
QY 1 CASELGKSTNTF 12  
||| |::|  
Db 1 CASSVALATEAF 12  
||| |::|

RESULT 8  
PT0217  
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C:Accession: PT0217  
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restri  
A:Reference number: PT0209; MUID:91217621; PMID:1902501  
A:Accession: PT0217  
A:Molecule type: mRNA

A;Residues: 1-11 <NAK>  
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 6  
||| ||  
Db 1 CASRLG 6

## RESULT 9

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C;Accession: S47391; S47386

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A;Reference number: S47355  
A;Accession: S47391  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-12 <LEH>  
A;Cross-references: EMBL:Z35712; NID:G527519; PIDN:CAA84781.1; PID:G527520; EMBL:Z35701;  
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12  
||| |  
Db 1 CASSGSGYGYTF 12

## RESULT 10

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C;Accession: S47383

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A;Reference number: S47355  
A;Accession: S47383  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-13 <LEH>  
A;Cross-references: EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PID:G527514  
C;Keywords: T-cell receptor

Query Match 37.5%; Score 27; DB 2; Length 13;  
Best Local Similarity 62.5%; Pred. No. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGKS 8  
||| :||  
Db 1 CASSMGGS 8

## RESULT 11

T cell receptor V-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)  
C;Date: 19-Oct-1995 #sequence\_revision 17-Nov-1995 #text\_change 05-Nov-1999  
C;Accession: S57575

R;Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P.

submitted to the EMBL Data Library, June 1995  
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A;Reference number: S57494

A;Accession: S57575

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <BUR>

A;Cross-references: EMBL:Z49953; NID:G887510; PIDN:CAA90224.1; PID:G887511

C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. No. 2.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKG 7  
||| :||  
Db 1 CASQGGK 7

## RESULT 12

S47395

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C;Accession: S47395

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A;Reference number: S47355

A;Accession: S47395

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-12 <LEH>

A;Cross-references: EMBL:Z35715; NID:G527525; PIDN:CAA84784.1; PID:G527526

C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12  
||| |  
Db 1 CASSQSGYGYTF 12

## RESULT 13

S47381

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C;Accession: S47381

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A;Reference number: S47355

A;Accession: S47381

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35698; NID:G527487; PIDN:CAA84767.1; PID:G527488

C;Keywords: T-cell receptor

Query Match 36.1%; Score 26; DB 2; Length 13;  
Best Local Similarity 41.7%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CASELKGKSTNTF 12  
||| :||  
Db 1 CASSTRSNTFAP 12

## RESULT 14

S47382

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
 C;Accession: S47382; S47370  
 R;Lehner, P.J.  
 submitted to the EMBL Data Library, August 1994  
 A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c  
 A;Reference number: S47355  
 A;Accession: S47382  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-13 <LEH>  
 A;Cross-references: EMBL:Z35687; NID:G527463; PIDN:CAA84756.1; PID:G527464; EMBL:Z35695;  
 C;Keywords: T-cell receptor

Query Match 35.4%; Score 25.5; DB 2; Length 13;  
 Best Local Similarity 54.5%; Pred. No. 3.6e+02;  
 Matches 6; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11  
 ||| : |||  
 Db 1 CASSM-RSTD 10

## RESULT 15

S23371  
 T-cell receptor alpha chain J region - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
 C;Accession: S23371  
 R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman  
 Eur. J. Immunol. 21, 2749-2754, 1991  
 A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu  
 A;Reference number: S23364; MUID:92037820; PMID:1657615  
 A;Accession: S23371  
 A;Status: preliminary; translation not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-10 <PLU>  
 A;Cross-references: EMBL:X58166  
 C;Keywords: T-cell receptor

Query Match 34.7%; Score 25; DB 2; Length 10;  
 Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9  
 : |||||  
 Db 2 SGEAGKST 9

Search completed: September 5, 2004, 10:32:20  
 Job time : 21 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:20:35 ; Search time 15 Seconds  
(without alignments)  
45.127 Million cell updates/sec

Title: US-09-761-636A-5  
Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 597

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	23	31.9	12	1	PSP3_PHYPA	P80662 physcomitre
2	20	27.8	12	1	V23K_WSSV	P82005 white spot
3	20	27.8	13	1	LIGA_TRAVE	P20011 trametes ve
4	20	27.8	13	1	PSPB_PINPS	P81668 pinus pinas
5	19	26.4	10	1	COXM_RAT	P80431 rattus norv
6	18	25.0	12	1	UR2B_CATCO	P04559 catostomus
7	18	25.0	13	1	FARB_ASCSU	P43173 ascaris suu
8	17	23.6	12	1	UR2B_CYPCA	P04561 cyprinus ca
9	16	22.2	9	1	XYLA_STRSQ	P19149 streptomyc
10	16	22.2	11	1	TKC2_CALVO	P41518 calliphora
11	16	22.2	12	1	CLX3_CONMR	P58809 conus maro
12	16	22.2	12	1	TA10_TREME	P01371 tremella me
13	16	22.2	13	1	CXAA_CONST	P28878 conus stria
14	16	22.2	13	1	HPB9_RANES	P32416 rana escul
15	15	20.8	9	1	CCAP_CARMA	P38556 carcinus ma
16	15	20.8	9	1	FAR5_ASCSU	P43170 ascaris suu
17	15	20.8	9	1	SAMP_MUSCA	P13095 mustelus ca
18	15	20.8	9	1	SAP_STOVA	P24047 stomopneute
19	15	20.8	10	1	COXQ_RABIT	P80336 oryctolagus
20	15	20.8	10	1	ODF2_BOVIN	P11180 bos taurus
21	15	20.8	11	1	CX5A_CONAL	P58848 conus aulic
22	15	20.8	11	1	CX5B_CONAL	P58849 conus aulic
23	15	20.8	11	1	FAR9_CALVO	P41864 calliphora
24	15	20.8	11	1	TIN1_HOPTI	P82651 hoplobatr
25	15	20.8	12	1	CXAI_CONIM	P50983 conus imper
26	15	20.8	12	1	NO40_LOTJA	O22426 lotus japon
27	15	20.8	12	1	SO15_BACSU	P80863 bacillus su
28	15	20.8	13	1	GER1_VESTR	P17231 vespa tropi
29	15	20.8	13	1	CXAI_CONGE	P01520 conus geogr
30	15	20.8	13	1	GER1_HORVU	P28525 hordeum vul
31	15	20.8	13	1	GER2_HORVU	P28526 hordeum vul
32	14	19.4	7	1	IGAO_DACDE	P06294 dactylium d
33	14	19.4	7	1	UC24_MAIZE	P80630 zea mays (m

34	14	19.4	9	1	FARB_MACRS	P83281 macrobrachi
35	14	19.4	10	1	LPK2_LOCMI	P41488 locusta mig
36	13	18.1	10	1	SYK_CAMUP	Q46464 campylobact
37	13	18.1	10	1	TKL4_LOCMI	P30250 locusta mig
38	13	18.1	10	1	TKNB_CHICK	P19851 gallus gall
39	13	18.1	10	1	TKNB_ONCMY	P28500 oncorhynch
40	13	18.1	10	1	TKNC_RANCA	P22690 rana catesb
41	13	18.1	10	1	URAG_HUMAN	P32080 homo sapien
42	13	18.1	10	1	VEGE_BACSU	P80699 bacillus su
43	13	18.1	12	1	UR2_POLSP	P81022 polyodon sp
44	13	18.1	13	1	CRBL_VESMA	P17232 vespa manda
45	13	18.1	13	1	ITB5_BOVIN	P80747 bos taurus

## ALIGNMENTS

RESULT 1  
PSP3\_PHYPA  
ID PSP3\_PHYPA STANDARD; PRT; 12 AA.  
AC P80662;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen  
evolving system of photosystem II) (Fragment).  
OS Physcomitrella patens (Moss).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;  
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.  
OX NCBI\_TaxID=3218;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Protonema;  
RX MEDLINE=97275459; PubMed=9129336;  
RA Kasten B., Buck F., Nuske J., Reski R.;  
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
plastid enzymes";  
RL Planta 201:261-272(1997).  
CC -!- FUNCTION: May be involved in the regulation of photosystem II.  
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated  
CC with the photosystem II complex.  
CC -!- INDUCTION: By light.  
CC -!- SIMILARITY: Belongs to the psbp family.  
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;  
KW Multigene family.  
FT NON\_TER 12  
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;  
Query Match 31.9%; Score 23; DB 1; Length 12;  
Best Local Similarity 57.1%; Pred. No. 3.2e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFF 12  
|:|:|  
Db 3 GESANVF 9

RESULT 2  
V23K\_WSSV  
ID V23K\_WSSV STANDARD; PRT; 12 AA.  
AC P82005;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE 23 kDa structural polypeptide (Fragment).  
OS White spot syndrome virus (WSSV).  
OC Viruses; dsDNA viruses, no RNA stage; Nimaviridae; Whispovirus.  
OX NCBI\_TaxID=92652;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=South Carolina;  
RX MEDLINE=20214217; PubMed=10752552;  
RA Wang Q., Poulos B.T., Lightner D.V.;

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RT "Protein analysis of geographic isolates of shrimp white spot syndrome
virus.";
RL Arch. Virol. 145:263-274 (2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON TER 12
SQ SEQUENCE 12 AA; 1323 MW; 0C0F41E91D51A724 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 ELGKSTN 10
| | |
DB 2 EFGNLTN 8

RESULT 3
LIGA TRAVE STANDARD; PRT; 13 AA.
AC P20011, 1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ligninase A (EC 1.11.1.14) (Diarylpropane peroxidase) (Lignin
peroxidase) (Fragment).
OS Trametes versicolor (White-rot fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxID=5325;
RN [1]
RP SEQUENCE.
RX MEDLINE=89211432; PubMed=2707445;
RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
RT "Trametes versicolor ligninase: isozyme sequence homology and
substrate specificity.";
RL FEBS Lett. 247:143-146 (1989).
CC -!- FUNCTION: Depolymerization of lignin. Catalyzes the C(alpha)-
C(beta) cleavage of the propyl side chains of lignin.
CC C(beta) cleavage of the propyl side chains of lignin.
CC -!- CATALYTIC ACTIVITY: 1,2-bis(3,4-dimethoxyphenyl)propane-1,3-diol +
H(2)O(2) = veratraldehyde + 1-(3,4-dimethylphenyl)ethane-1,2-diol
+ 4 H(2)O.
CC -!- PATHWAY: Lignin degradation; first step.
CC -!- SIMILARITY: Belongs to the peroxidase family. Ligninase subfamily.
DR PIR; S04013; S04013.
DR InterPro; IPR002016; Peroxidase.
DR PROSITE; PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE; PS00436; PEROXIDASE_2; PARTIAL.
DR Oxidoreductase; Peroxidase; Iron; Heme; Glycoprotein;
KW Multigene family; Lignin degradation.
FT NON TER 13
SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GKSTNT 11
| | |
DB 6 GKNTAT 11

RESULT 4
PSPB_PINPS STANDARD; PRT; 13 AA.
AC P81668;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (23 kDa subunit of oxygen
evolving system of photosystem II) (Fragment).
DE PSPB.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RX TISSUE=Needle;
RC MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins.";
RL Electrophoresis 20:1098-1108 (1999).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein
CC (spot N179) is: 5.9, its MW is: 22 kDa.
CC -!- SIMILARITY: Belongs to the psbp family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.
FT NON TER 13
SQ SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;

Query Match 27.8%; Score 20; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTF 12
| | |
DB 3 GEANVF 9

RESULT 5
COXM RAT STANDARD; PRT; 10 AA.
ID _COXM_RAT
AC P80431;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide Viib, mitochondrial (EC 1.9.3.1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
amino-terminal sequences suggest identity of the fetal heart and the
adult liver isoform.";
RL Eur. J. Biochem. 230:235-241 (1995).
CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC PIR; S65387; S65387.
DR Oxidoreductase; Mitochondrion.
KW NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 26.4%; Score 19; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 KSTNTF 12
| | |
DB 4 KKTPTF 9

RESULT 6

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UR2B_CATCO
ID UR2B_CATCO STANDARD; PRT; 12 AA.
AC P04559;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin IIB (U-IIB) (UIIB).
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Catostomidae; Catostomus.
OX NCBI_TaxID=7971;
RN [1]
SEQUENCE.
RX MEDLINE=84041959; PubMed=6138759;
RA McMaster D., Lederis K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373(1983).
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the urotensin 2 family.
DR PIR; JS0424; JS0424.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1437 MW; 73961BDB879CEBB CRC64;

Query Match 25.0%; Score 18; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 TMTFC 13
Db :|||
2 SNTFC 6

RESULT 7
FARB_ASCSU
ID FARB_ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation.
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D686B05 CRC64;

Query Match 25.0%; Score 18; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 SELGKSTNWF 12
Db :|||
1 SDIGISEPNF 10

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RESULT 8
UR2B_CYPCA
ID UR2B_CYPCA STANDARD; PRT; 12 AA.
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Urotensin II-beta (UII-beta) (U-II-beta).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
SEQUENCE.
RA MuneKata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RL (In) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72,
RL Pierce Chemical Co., Rockford IL. (1981).
CC -!- FUNCTION: Urotensin is found in the teleost caudal neurosecretory
CC system. It has a suggested role in osmoregulation and as a
CC corticotropin-releasing factor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the urotensin 2 family.
DR InterPro; IPR001483; Urotensin II.
DR Pfam; PF02083; Urotensin II; 1.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
FT VARIANT 2 12 G -> S.
SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;

Query Match 23.6%; Score 17; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 NTFC 13
Db :|||
3 NTEC 6

RESULT 9
XYLA_STRSQ
ID XYLA_STRSQ STANDARD; PRT; 9 AA.
AC P19149;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYLA.
OS Streptomyces sp. (strain NCL 82-5-1).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1931;
RN [1]
SEQUENCE.
RX MEDLINE=88326335; PubMed=3415697;
RA Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;
RT "Purification and characterisation of glucose (xylose) isomerase from
RT Chainia sp. (NCL 82-5-1).";
RL Biochem. Biophys. Res. Commun. 155:411-417(1988).
CC -!- FUNCTION: Involved in D-xylose catabolism.
CC -!- CATALYTIC ACTIVITY: D-xylose = D-xylulose.
CC -!- COFACTOR: Binds 2 magnesium ions per subunit (Potential).
CC -!- SUBUNIT: Homotetramer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the xylose isomerase family.
DR PIR; A31576; A31576.
DR HAMAP; MF_00455; -.
DR InterPro; IPR001998; Xylose_isom.
DR PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.

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DR PROSITE: PS00173; XYLOSE ISOMERASE 2; PARTIAL.  
 KW Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.  
 FT NON\_TER 9  
 SQ SEQUENCE 9 AA; 983 MW; F64BA1EDC5B87DD1 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 8 STNTP 12  
 Db 5 SAHTP 9

RESULT 10  
 TKC2\_CALVO STANDARD; PRT; 11 AA.  
 AC P415T8;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Callitachykinin II.  
 OS Calliphora vomitoria (Blue blowfly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 OC Calliphoridae; Calliphora.  
 OX NCBI\_TaxID=27454;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95075727; PubMed=7984492;  
 RA Lundquist C.T., Clottens F.L., Holman G.M., Nichols R., Nachman R.J.,  
 RA Naessel D.R.;  
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from  
 RT the blowfly, Calliphora vomitoria, that have resemblances to  
 RT tachykinins."  
 RL Peptides 15:761-768(1994).  
 CC -|- FUNCTION: Myoactive peptide.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.  
 KW Tachykinin; Neuropeptide; Amidation.  
 FT MOD\_RES 11  
 SQ SEQUENCE 11 AA; 1103 MW; 15D7E3F9C9CDB444 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 11;  
 Best Local Similarity 42.9%; Pred. No. 5.7e+03;  
 Matches 3; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 6 GKSTNTP 12  
 Db 1 GLGNAP 7

RESULT 11  
 CXL3\_CONMR STANDARD; PRT; 12 AA.  
 AC P58809;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lambda-conotoxin CmrX.  
 OS Conus marmoreus (Marble cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=42752;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20564325; PubMed=10988292;  
 RA Balaji R.A., Ohake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
 RA Seow K.T., Bay B.-H.;  
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
 pattern and protein folding. Isolation and characterization from the

RT venom of Conus marmoreus.";  
 RL J. Biol. Chem. 275:39516-39522(2000).  
 CC -|- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -|- MASS SPECTROMETRY: MW=1262.77; MW ERR=0.07; METHOD=Electrospray.  
 CC -|- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
 KW Neurotoxin; Toxin; Hydroxylation.  
 FT DISULFID 3 12  
 FT DISULFID 4 9  
 FT MOD\_RES 11 11  
 SQ SEQUENCE 12 AA; 1251 MW; 277AAAE2422D5A2C8 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 11 TFC 13  
 Db 7 SFC 9

RESULT 12  
 TAL0\_TREME STANDARD; PRT; 12 AA.  
 AC P01371;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Tremorgen A-10.  
 OS Tremella mesenterica (Jelly fungus).  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
 OC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.  
 OX NCBI\_TaxID=5217;  
 RN [1]  
 RP SAKAGAMI.  
 RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;  
 RT "Peptide sex hormones inducing conjugation tube formation in  
 RT compatible mating-type cells of Tremella mesenterica."  
 RL Science 212:1525-1527(1981).  
 CC -|- FUNCTION: Tremorgen A-10 is produced by the a mating-type cells  
 CC and induces formation of conjugation tubes in a mating-type cells.  
 DR PIR; A01642; JTJGO.  
 KW Lipoprotein; Prenylation; Methylation; Pheromone.  
 FT LIPID 12 12  
 FT MOD\_RES 12 12  
 SQ SEQUENCE 12 AA; 1246 MW; 84EF574959676DC5 CRC64;

Query Match 22.2%; Score 16; DB 1; Length 12;  
 Best Local Similarity 50.0%; Pred. No. 6.2e+03;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 NTFC 13  
 Db 9 NGYC 12

RESULT 13  
 CXAA\_CONST STANDARD; PRT; 13 AA.  
 AC P28878;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin SIA (SIA).  
 OS Conus striatus (Striated cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6493;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;

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RX MEDLINE=91369955; PubMed=1892838;
RA Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA Oliveira B.M.;
RT "Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT receptors.";
RL Biochemistry 30:9370-9377(1991).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR: A40312; NTKNAS.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation.
FT DISULFID 2 7
FT DISULFID 3 13
FT MOD RES 13 13
FT MOD RES 13 13
SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457EBD CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 37.5%; Pred.No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGS 8
Db 3 CHPACGKN 10

RESULT 14
HPB9 RANES STANDARD; PRT; 13 AA.
AC P32416;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hemolytic protein B9 (Fragment).
OS Rana esculenta (Edible frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8401;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90198965; PubMed=2317508;
RA Simmaco M., de Biase D., Severini C., Aita M., Erspamer G.F.,
RA Barra D., Bossa F.;
RT "Purification and characterization of bioactive peptides from skin
RT extracts of Rana esculenta.";
RL Biochim. Biophys. Acta 1033:318-323(1990).
CC -!- FUNCTION: Shows hemolytic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
DR PIR: S09019; S09019.
KW Amphibian defense peptide; Amidation; Hemolysis.
FT MOD RES 13 13
FT NON RES 13 13
FT NON RES 13 13
SQ SEQUENCE 13 AA; 1402 MW; C6B41A765DF9287D CRC64;

Query Match 22.2%; Score 16; DB 1; Length 13;
Best Local Similarity 56.7%; Pred.No. 6.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGK 7
Db 6 AGLGK 11

RESULT 15
CCAP CARMA STANDARD; PRT; 9 AA.
ID CCAP CARMA
AC P38556;

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DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
OS Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C.maenas; TISSUE=Pericardial organs;
RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
RT shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M.sexata; PubMed=1426284;
RX MEDLINE=93050243;
RA Cheung C.-C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
RT hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
RA Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
RT molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released
CC into the hemolymph.
DR PIR: A26363; A26363.
DR PIR: S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD RES 9 9
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 20.8%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 FC 13
Db 2 FC 3

Search completed: September 5, 2004, 10:30:49
Job time : 16 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:22:06 ; Search time 57 Seconds  
(without alignments)  
71.960 Million cell updates/sec

Title: US-09-761-636A-5  
Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3001

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phase.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	37.5	13	13 Q8QZ5	Q8QZ5 fugu rubrip
2	26	36.1	13	12 Q9184	Q9184 human papil
3	26	36.1	13	12 Q9186	Q9186 human papil
4	23	31.9	12	13 Q9PS67	Q9PS67 gallus gall
5	21	29.2	12	12 Q85666	Q85666 reovirus (t
6	21	29.2	13	6 Q9GTU2	Q9GTU2 ovis aries
7	21	29.2	13	13 P82821	P82821 rana catesb
8	21	29.2	13	13 P82822	P82822 rana catesb
9	20	27.8	11	10 Q9T0L9	Q9T0L9 brassica ol
10	20	27.8	12	3 Q9UR22	Q9UR22 cryptococu
11	20	27.8	12	13 P82820	P82820 rana catesb
12	20	27.8	13	11 Q80W20	Q80W20 rattus sp.
13	20	27.8	13	13 P82823	P82823 rana catesb
14	19	26.4	12	11 Q61331	Q61331 mus musculu
15	19	26.4	13	11 Q54809	Q54809 mus musculu
16	18	25.0	8	7 Q95213	Q95213 oryctolagus

17	18	25.0	11	9	Q37925	Q37925 bacterioph
18	18	25.0	11	13	Q9PS71	Q9PS71 agkistrodon
19	18	25.0	12	6	Q7YS46	Q7YS46 ovis aries
20	18	25.0	12	8	Q7YKE9	Q7YKE9 ribes divar
21	18	25.0	13	4	Q9UDC6	Q9UDC6 homo sapien
22	18	25.0	13	13	P82881	P82881 rana clamit
23	17	23.6	11	2	Q9EUZ3	Q9EUZ3 escherichia
24	17	23.6	11	4	Q9HCN5	Q9HCN5 homo sapien
25	17	23.6	12	5	Q8T0Y6	Q8T0Y6 apis mellif
26	17	23.6	12	6	Q9BFV4	Q9BFV4 myrmecophag
27	17	23.6	12	8	Q7YKC9	Q7YKC9 ribes speci
28	17	23.6	13	4	Q13377	Q13377 homo sapien
29	17	23.6	13	11	Q35758	Q35758 rattus norv
30	16	22.2	8	2	Q7X139	Q7X139 staphylococ
31	16	22.2	9	2	Q30790	Q30790 erwinia amy
32	16	22.2	9	4	Q15999	Q15999 homo sapien
33	16	22.2	9	12	Q88612	Q88612 middelburg
34	16	22.2	10	4	Q8NEY9	Q8NEY9 homo sapien
35	16	22.2	10	6	Q9TRU6	Q9TRU6 bos taurus
36	16	22.2	11	11	P97330	P97330 mus musculu
37	16	22.2	11	11	Q9RLN6	Q9RLN6 mus musculu
38	16	22.2	12	2	Q9S550	Q9S550 streptococ
39	16	22.2	12	5	Q17140	Q17140 crassostrea
40	16	22.2	12	5	Q26429	Q26429 drosophila
41	16	22.2	12	11	Q64242	Q64242 rattus sp.
42	16	22.2	13	4	Q9UMK9	Q9UMK9 homo sapien
43	16	22.2	13	4	Q9GQ66	Q9GQ66 homo sapien
44	16	22.2	13	5	Q818F2	Q818F2 drosophila
45	16	22.2	13	5	Q818F1	Q818F1 drosophila

## ALIGNMENTS

## RESULT 1

Q8QZ5	PRELIMINARY;	PRT;	13 AA.
ID	Q8QZ5		
AC	Q8QZ5;		
DT	01-JUN-2002 (TREMBLrel. 21, Created)		
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)		
DE	Guanine nucleotide binding protein (Fragment).		
GN	GNAO.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Takifugu.		
OX	NCBI_TaxID=31033;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97129408; PubMed=8973916;		
RA	Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;		
RT	"G protein alpha subunit multigene family in the Japanese puffer fish		
RT	Fugu rubripes; PCR from a compact vertebrate genome.";		
RL	Genome Res. 6:1207-1215(1996).		
DR	EMBL; L79891; AAL77640.1;		
DR	GO; GO:0004871; F:signal transducer activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.		
DR	InterPro; IPR001019; Gprotein_alpha.		
DR	Pfam; PF00503; G-alpha; 1.		
FT	NON_TER 1		
FT	NON_TER 13		
SQ	SEQUENCE 13 AA; 1336 MW; 465B59640B44B5B3 CRC64;		

Query Match 37.5%; Score 27; DB 13; Length 13;  
Best Local Similarity 75.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9  
Db 1 AGESGKST 8

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RESULT 2
Q918T4 PRELIMINARY; PRT; 13 AA.
AC Q918T4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OC NCBI_TaxID=10581;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC7;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407220; AAL01406.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 3
Q918T6 PRELIMINARY; PRT; 13 AA.
AC Q918T6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407219; AAL01403.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 36.1%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 5.6e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 4
Q9P867 PRELIMINARY; PRT; 12 AA.
AC Q9P867;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Myosin (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=92031443; PubMed=1931944;
RA Garabedian T.B., Yount R.G.;
RT "Direct photoaffinity labeling of gizzard myosin with vanadate-trapped
RT adenosine diphosphate.";
RL Biochemistry 30:10126-10132(1991).
DR PIR; A23695; A23695.
FT NON TER 1
SQ SEQUENCE 12 AA; 1178 MW; C1FC2E0D9AA3387D CRC64;

Query Match 31.9%; Score 23; DB 13; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SELGKSTNT 11
DB 3 SGAGKTENT 11

RESULT 5
Q85666 PRELIMINARY; PRT; 12 AA.
AC Q85666;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Reovirus serotype 3 M3 (Fragment).
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
OX NCBI_TaxID=10886;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017876; PubMed=6927854;
RA Antczak J.B., Chmelo R., Pickup D.J., Joklik W.K.;
RT "Sequences at both termini of the 10 genes of reovirus serotype 3
RT (strain Dearing).";
RL Virology 121:307-319(1982).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017877; PubMed=7123853;
RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus
RT serotypes.";
RL Virology 121:320-326(1982).
DR EMBL; J02323; AAA47259.1; -.
FT NON TER 12
SQ SEQUENCE 12 AA; 1275 MW; 4B292B17FCB9C873 CRC64;

Query Match 29.2%; Score 21; DB 12; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ASELGKSTNT 11
DB 2 ASFKGFSANT 11

RESULT 6
Q9GJU2 PRELIMINARY; PRT; 13 AA.
AC Q9GJU2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

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DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Nonneman D., Geesink G.H., Koohmaraie M.;
RT "Differential splicing and protein isoforms of ovine calpastatin.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF192536; AAG31688.1; -.
DR EMBL; AF192535; AAG31687.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1335 MW; 47E9542C696BADD3 CRC64;

Query Match 29.2%; Score 21; DB 6; Length 13;
Best Local Similarity 80.0%; Pred. No. 5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GKSTN 10
DB 9 GKSTS 13

RESULT 7
P82821 ID P82821 PRELIMINARY; PRT; 13 AA.
AC P82821;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RANATUERIN 6.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480BD0CF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 8
P82822 ID P82822 PRELIMINARY; PRT; 13 AA.
AC P82822;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE RANATUERIN 7.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8400;

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RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Goraya J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
DR GO; GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1398 MW; C85480BD0CF885BD CRC64;

Query Match 29.2%; Score 21; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
DB 6 ASMLGK 11

RESULT 9
Q9T0L9 ID Q9T0L9 PRELIMINARY; PRT; 11 AA.
AC Q9T0L9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN SLG5.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Caballiac D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaude T., Cock J.M.;
RT "The S15, self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986 (1999).
DR EMBL; Y18256; CAB41875.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 27.8%; Score 20; DB 10; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9
DB 3 AADLGTCT 10

RESULT 10
Q9UR22 ID Q9UR22 PRELIMINARY; PRT; 12 AA.
AC Q9UR22;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE STE12 alpha (Fragment).
GN STE12ALPHA.
OS Cryptococcus neoformans var. neoformans.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=40410;
RN [1]

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Sun Sep 5 11:41:12 2004

us-09-761-636a-5.closed.rspt

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RP SEQUENCE FROM N.A.
RC STRAIN=CB5884, BAL 3, and CBS6989;
RX MEDLINE=99380307; PubMed=1049476;
RA Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
RA Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
RT collections of Cryptococcus neoformans var. gattii strains from
RT Australia.";
RL J. Clin. Microbiol. 37:2920-2926 (1999).
DR EMBL; AF155349; AAF20374.1; -
DR EMBL; AF155347; AAF20372.1; -
DR EMBL; AF155348; AAF20373.1; -
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1307 MW; 5AF9B485D5A735B7 CRC64;

Query Match 27.8%; Score 20; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TFC 13
Db 8 TFC 10

RESULT 11
P82820 PRELIMINARY; PRT; 12 AA.
AC P82820;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE RANATUERIN 5.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- SUBCELLULAR LOCATION: SECRETED.
SQ SEQUENCE 12 AA; 1335 MW; C8531D12A92735BD CRC64;

Query Match 27.8%; Score 20; DB 13; Length 12;
Best Local Similarity 83.3%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
Db 5 ASLLGK 10

RESULT 12
Q80WZ0 PRELIMINARY; PRT; 13 AA.
AC Q80WZ0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE GTP-binding protein Golf alpha subunit (Fragment).
GN G-ALPHA-OLF.
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96115117; PubMed=7494450;

RA Herve D., Rogard M., Levi-Strauss M.;
RT "Molecular analysis of the multiple Golf alpha subunit mRNAs in the
RT rat brain.";
RL Brain Res. 32:125-134 (1995).
DR EMBL; S80330; AAP32222.1; -
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1312 MW; 0B6E3319671CA5B4 CRC64;

Query Match 27.8%; Score 20; DB 11; Length 13;
Best Local Similarity 57.1%; Pred. No. 7.7e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LGKSTNT 11
Db 4 LGSSKT 10

RESULT 13
P82823 PRELIMINARY; PRT; 13 AA.
AC P82823;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RANATUERIN 8.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=SKIN;
RX MEDLINE=98422096; PubMed=9751476;
RA Gorava J., Knoop F.C., Conlon J.M.;
RT "Ranaturins: antimicrobial peptides isolated from the skin of the
RT American bullfrog, Rana catesbeiana.";
RL Biochem. Biophys. Res. Commun. 250:589-592 (1998).
CC -!- FUNCTION: ANTIBACTERIAL PEPTIDE AGAINST GRAM-NEGATIVE BACTERIUM
CC S.AUREUS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC GO: GO:0006805; P: xenobiotic metabolism; IEA.
KW Antibiotic.
SQ SEQUENCE 13 AA; 1414 MW; C85480BD0CF7D5BD CRC64;

Query Match 27.8%; Score 20; DB 13; Length 13;
Best Local Similarity 83.3%; Pred. No. 7.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGK 7
Db 6 ASFLGK 11

RESULT 14
Q61331 PRELIMINARY; PRT; 12 AA.
AC Q61331;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE N-acetylglucosamine (Beta1-4) galactosyl transferase (EC 2.4.1.90)
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89033997; PubMed=3141392;
RA Nakazawa K., Ando T., Kimura T., Narimatsu H.;
RT "Cloning and sequencing of a full-length cDNA of mouse N-
RT acetylglucosamine (beta1-4) galactosyltransferase.";
RL J. Biochem. 104:165-168 (1988).

```

Search completed: September 5, 2004, 10:31:54  
Job time : 59 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:01:30 ; Search time 65 Seconds  
(without alignments)  
56.510 Million cell updates/sec

Title: US-09-761-636A-5  
Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 383904

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	13	4	AAU04524
2	69	95.8	13	4	AAU04534
3	65	90.3	13	4	AAU04535
4	65	90.3	13	4	AAU04537
5	61	84.7	13	4	AAU04536
6	32	44.4	12	3	AAU04536
7	32	44.4	13	5	ABJ04094
8	30	41.7	13	3	AAU04094
9	29	40.3	10	4	AAU04094
10	29	40.3	13	3	AAU04094
11	29	40.3	13	5	AAU04094
12	28	38.9	9	2	AAU04094
13	28	38.9	9	3	AAU04094
14	28	38.9	9	5	AAU04094
15	28	38.9	10	3	AAU04094
16	28	38.9	13	5	AAU04094
17	28	38.9	13	5	AAU04094
18	27	37.5	9	5	AAU04094
19	27	37.5	10	2	AAU04094
20	27	37.5	10	4	AAU04094
21	27	37.5	12	2	AAU04094
22	27	37.5	12	2	AAU04094
23	27	37.5	12	4	AAU04094
24	27	37.5	12	4	AAU04094
25	27	37.5	12	5	AAU04094

26	27	37.5	12	6	ADA23476
27	27	37.5	13	3	AAB26567
28	27	37.5	13	4	AAU16900
29	27	37.5	13	5	ABJ00485
30	27	37.5	13	5	ABJ04090
31	27	37.5	13	5	ABJ04092
32	27	37.5	13	5	ABJ04093
33	26	36.1	8	4	AAU08458
34	26	36.1	9	2	AAW83264
35	26	36.1	9	2	AAW67159
36	26	36.1	9	2	AAW97980
37	26	36.1	9	3	AAU76718
38	26	36.1	9	6	ABP74688
39	26	36.1	9	7	ADC09547
40	26	36.1	10	4	AAW84316
41	26	36.1	10	4	AAW96997
42	26	36.1	10	4	AAW96549
43	26	36.1	10	5	ABP47552
44	26	36.1	10	6	ABP74689
45	26	36.1	10	7	ADC09548

## ALIGNMENTS

RESULT 1  
ID AAU04524 standard; peptide; 13 AA.  
XX  
AC AAU04524;  
XX  
DT 26-SEP-2001 (first entry)  
XX  
DE VEGF based monocyclic peptide 1.  
XX  
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1..13  
XX  
XX /note= "This bond cyclises the peptide"  
XX  
XX WO200152875-A1.  
XX  
XX 26-JUL-2001.  
XX  
XX 18-JAN-2001; 2001WO-US001533.  
XX  
XX 18-JAN-2000; 2000US-0176293P.  
XX  
XX 16-MAY-2000; 2000US-0204590P.  
XX  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX  
XX Achen MG, Hughes RA, Stacker S, Cendron A;  
XX  
XX WPI; 2001-442248/47.  
XX  
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
XX from an exposed loop of a growth factor protein by oxidizing the cysteine  
XX residues.  
XX  
XX Claim 49; Page 32; 102pp; English.  
XX  
XX The sequence represents a monomeric monocyclic peptide of the invention,  
XX whose 3-dimensional structure is modelled on the exposed loop of human  
XX VEGF (vascular endothelial growth factor). The invention relates to a  
XX method of producing a monomeric monocyclic peptide by a measuring beta-  
XX beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 13 AA;

Query Match 100.0%; Score 72; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
 |||||  
 Db 1 CASELGKSTNTFC 13

RESULT 2  
 AAU04534  
 ID AAU04534 standard; peptide; 13 AA.  
 XX  
 AC AAU04534;  
 XX  
 XX 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based monocyclic peptide 12.  
 XX  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 XX Disulfide-bond 1..13  
 FT /note= "This bond cyclises the peptide"  
 XX  
 XX WO200152875-A1.  
 XX  
 XX 26-JUL-2001.  
 XX  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX  
 XX 18-JAN-2000; 2000US-0176293P.  
 XX 16-MAY-2000; 2000US-0204590P.  
 XX  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX  
 XX WPI; 2001-442248/47.  
 XX

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 XX from an exposed loop of a growth factor protein by oxidising the cysteine  
 XX

PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 XX  
 CC The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 13 AA;

Query Match 95.8%; Score 69; DB 4; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 6.8e-05;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
 |||||  
 Db 1 CASELGKSTNTFC 13

RESULT 3  
 AAU04535  
 ID AAU04535 standard; peptide; 13 AA.  
 XX  
 AC AAU04535;  
 XX  
 XX 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based monocyclic peptide 13.  
 XX

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers  
 XX Disulfide-bond 1..13  
 FT /note= "This bond cyclises the peptide"  
 XX

XX WO200152875-A1.  
 XX  
 XX 26-JUL-2001.  
 XX  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX  
 XX 18-JAN-2000; 2000US-0176293P.  
 XX 16-MAY-2000; 2000US-0204590P.  
 XX

```

PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stacker S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Example 25; Page 47; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 13 AA;
XX
XX Query Match 90.3%; Score 65; DB 4; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 0.00033;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CASELGKSTNTFC 13
XX |||||:|||||
XX Db 1 CASELGKSTNTFC 13
XX
XX RESULT 4
XX AAU04537
XX ID AAU04537 standard; peptide; 13 AA.
XX
XX AC AAU04537;
XX
XX DT 26-SEP-2001 (first entry)
XX
XX DE VEGF based monocyclic peptide 15.
XX
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX Disulfide-bond 1..13
XX FT /note= "This bond cyclises the peptide"
XX

```

```

PN WO200152875-A1.
XX
XX PD 26-JUL-2001.
XX
XX PF 18-JAN-2001; 2001WO-US001533.
XX
XX PR 18-JAN-2000; 2000US-0176293P.
XX
XX PR 16-MAY-2000; 2000US-0204590P.
XX
XX XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX PA Achen MG, Hughes RA, Stacker S, Cendron A;
XX PI WPI; 2001-442248/47.
XX
XX DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX PS Example 25; Page 47; 102pp; English.
XX
XX CC The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGFD (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis,
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX CC Sequence 13 AA;
XX
XX Query Match 90.3%; Score 65; DB 4; Length 13;
XX Best Local Similarity 84.6%; Pred. No. 0.00033;
XX Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CASELGKSTNTFC 13
XX |||||:|||||
XX Db 1 CASELGKSTNTFC 13
XX
XX RESULT 5
XX AAU04536
XX ID AAU04536 standard; peptide; 13 AA.
XX
XX AC AAU04536;
XX
XX DT 26-SEP-2001 (first entry)
XX
XX DE VEGF based monocyclic peptide 14.
XX
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;

```

ID AAY57039 standard; peptide; 12 AA.



XX 08-NOV-2001; 2001WO-EF012933.  
 XX  
 PR 08-NOV-2000; 2000EP-00124418.  
 XX  
 XX (AFFI-) AFFINA IMMUNTECHNIK GMBH.  
 XX  
 PI Egner R, Winkler D, Roenspeck W, Kunze R;  
 XX  
 XX WPI; 2002-557447/59.  
 DR  
 XX  
 XX New immunoglobulin-binding peptides, useful for removing autoantibodies  
 PT from serum, e.g. for treating rheumatism, also related solid phases.  
 PT  
 XX  
 XX Claim 3; Page 40; 54pp; German.  
 PS  
 XX  
 XX The present invention relates to immunoglobulin binding peptides. These  
 CC can be used to remove autoantibodies from solutions, particularly  
 CC autoantibodies associated with autoimmune diseases such as rheumatism,  
 CC multiple sclerosis and myasthenia gravis, from body fluids. The present  
 CC sequence is a peptide of the invention  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 44.4%; Score 32; DB 5; Length 13;  
 Best Local Similarity 85.7%; Pred. No. 1.4e+02;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7  
 DB |||||  
 2 CASHLOK 8

RESULT 8  
 AAY66781  
 ID AAY66781 standard; peptide; 13 AA.  
 XX  
 AC AAY66781;  
 XX  
 DT 11-APR-2000 (first entry)  
 XX  
 DE T cell antigen receptor Vbeta 5 chain peptide.  
 XX  
 DE Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;  
 KW Vbeta chain; autoantigen; immunological tolerance.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO9963084-A1.  
 PN  
 XX 09-DEC-1999.  
 PD  
 XX 28-MAY-1999; 99WO-JP002814.  
 PF  
 XX 29-MAY-1998; 98JP-00149855.  
 PR  
 XX 14-OCT-1998; 98JP-00328761.  
 FR  
 XX (TORI) TORII PHARM CO LTD.  
 PA  
 XX Nishioka K, Yoshino S;  
 PI  
 XX WPI; 2000-086978/07.  
 DR  
 XX N-PSDB; AA296511.  
 DR  
 XX T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in  
 PT synovial membranes of rheumatoid arthritis patients.  
 PT  
 XX Example 3; Page 25; 136pp; Japanese.  
 PS  
 XX The invention relates to peptide sequences present in the synovial fluid  
 CC and membranes of rheumatoid arthritis patients, arising from the CDR  
 CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.  
 CC Compositions which contain autoantigenic peptides binding specifically to

CC T-cells expressing receptors containing the peptide sequences, which  
 CC include antigen-specific immunological tolerance to rheumatoid arthritis  
 CC can be used for the treatment and prevention of rheumatoid arthritis. The  
 CC invention can be used for the diagnosis, treatment and prevention of  
 CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the  
 CC various Vbeta chains of T cell antigen receptor  
 XX  
 XX Sequence 13 AA;  
 SQ

Query Match 41.7%; Score 30; DB 3; Length 13;  
 Best Local Similarity 41.7%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTP 12  
 DB |||||  
 2 CASSIGTNEQF 13

RESULT 9  
 AAB75626  
 ID AAB75626 standard; peptide; 10 AA.  
 XX  
 AC AAB75626;  
 XX  
 DT 10-APR-2001 (first entry)  
 XX  
 DE HLA class I binding motif in HOM-TES-84 SEQ ID NO:29.  
 XX  
 KW Human; cancer associated antigen precursor; cancer associated antigen;  
 KW seminoma; HLA; human leukocyte antigen; cytostatic; gene therapy;  
 KW vaccine; cancer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200100874-A2.  
 PN  
 XX 04-JAN-2001.  
 PD  
 XX 23-JUN-2000; 2000WO-US017207.  
 PF  
 XX 30-JUN-1999; 99US-00346498.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Sahin U, Tureci O, Pfreundschuh M;  
 PI  
 XX WPI; 2001-112465/12.  
 DR  
 XX Diagnosing a disorder characterized by expression of a human cancer  
 PT associated antigen precursor, comprises detecting interaction of an agent  
 PT with a nucleic acid molecule encoding the antigen precursor.  
 XX  
 PS Example 10; Page 62; 136pp; English.  
 XX  
 XX The present invention describes a method for diagnosing a disorder  
 CC characterised by expression of a human cancer associated antigen (CAA)  
 CC precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) comprising  
 CC contacting the biological sample with an agent (A) that specifically  
 CC binds to N1, (I) or its fragment, complexed with an human leukocyte  
 CC antigen (HLA) molecule and determining the interaction between the agent  
 CC and N1 or (I). (I) has cytostatic activity and can be used in gene  
 CC therapy and vaccine production. The method can be used for treating a  
 CC subject with a condition characterised by expression of (I) in cells of a  
 CC subject. AAB75607 and AAB75608 represent proteins from human cancer  
 CC associated antigen precursors, and AAB75609 to AAB75802 represent HLA  
 CC class I binding motifs in human cancer associated antigen precursors  
 CC given in the exemplification of the present invention  
 XX  
 XX Sequence 10 AA;  
 SQ

Query Match 40.3%; Score 29; DB 4; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

QY      4 ELKSTNTFC 13
DB      1 KLGSFNTNC 10

RESULT 10
AAY66787
ID AAY66787 standard; peptide; 13 AA.
XX
AC AAY66787;
XX
DT 11-APR-2000 (first entry)
XX
DE T cell antigen receptor Vbeta 10 chain peptide.
XX
KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
KW Vbeta chain; autoantigen; immunological tolerance.
XX
OS Homo sapiens.
XX
PN WO963084-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002814.
XX
PR 29-MAY-1998; 98JP-00149855.
XX
PR 14-OCT-1998; 98JP-00328761.
XX
PA (TORI ) TORII PHARM CO LTD.
XX
PI Nishioka K, Yoshino S;
XX
DR WPI; 2000-086978/07.
XX
DR N-PSDB; AA296517.
XX
PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
PT synovial membranes of rheumatoid arthritis patients.
XX
PS Example 3; Page 29; 136pp; Japanese.
XX
CC The invention relates to peptide sequences present in the synovial fluid
CC and membranes of rheumatoid arthritis patients, arising from the CDR
CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
CC Compositions which contain autoantigenic peptide binding specifically to
CC T-cells expressing receptors containing the peptide sequences, which
CC include antigen-specific immunological tolerance to rheumatoid arthritis
CC can be used for the treatment and prevention of rheumatoid arthritis. The
CC invention can be used for the diagnosis, treatment and prevention of
CC rheumatoid arthritis. Sequences AAY66771-958 represent peptides from the
CC various Vbeta chains of T cell antigen receptor
XX
SQ Sequence 13 AA;
Query Match 40.3%; Score 29; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CASELGKST 9
DB      2 CASSKGTST 10

RESULT 11
ABJ04095
ID ABJ04095 standard; peptide; 13 AA.
XX
AC ABJ04095;
XX
DT 01-OCT-2002 (first entry)
XX
DE Immunoglobulin binding peptide #15.

```

```

XX Immunoglobulin binding peptide; autoimmune disease; rheumatoid arthritis;
KW multiple sclerosis; myasthenia gravis; immunosuppressive; antirheumatic;
KW neuroprotective.
XX
OS Synthetic.
XX
PN WO200238592-A2.
XX
PD 16-MAY-2002.
XX
PF 08-NOV-2001; 2001WO-EP012933.
XX
PR 08-NOV-2000; 2000EP-00124418.
XX
PA (AFFI-) AFFINA IMMUNTECHNIK GMBH.
XX
PI Egner R, Winkler D, Roenspeck W, Kunze R;
XX
DR WPI; 2002-557447/59.
XX
PT New immunoglobulin-binding peptides, useful for removing autoantibodies
PT from serum, e.g. for treating rheumatism, also related solid phases.
XX
PS Claim 3; Page 40; 54pp; German.
XX
CC The present invention relates to immunoglobulin binding peptides. These
CC can be used to remove autoantibodies from solutions, particularly
CC autoantibodies associated with autoimmune diseases such as rheumatism,
CC multiple sclerosis and myasthenia gravis, from body fluids. The present
CC sequence is a peptide of the invention
XX
SQ Sequence 13 AA;
Query Match 40.3%; Score 29; DB 5; Length 13;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CASELGK 7
DB      2 CATHLGK 8

RESULT 12
AAY48678
ID AAY48678 standard; peptide; 9 AA.
XX
AC AAY48678;
XX
DT 20-MAR-2003 (revised)
DT 10-DEC-1999 (first entry)
XX
DE Membrane dipeptidase-binding lung homing peptide #49.
XX
KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
KW membrane dipeptidase.
XX
OS Synthetic.
XX
OS Homo sapiens.
XX
PN WO9946284-A2.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US005284.
XX
PR 13-MAR-1998; 98US-00042107.
XX
PR 26-FEB-1999; 99US-00258754.
XX
PA (BURN-) BURNHAM INST.
XX
PI Rajotte D, Pasqualini R, Ruoslahti EI;

```

XX WPI; 1999-571717/48.  
 XX New peptides which selectively home to organs or tissues, used for, e.g.  
 PT identifying target ligands and for therapy of pathological conditions.  
 XX Example 6; Page 144; 193pp; English.  
 XX The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)  
 XX Sequence 9 AA;  
 SQ Query Match 38.9%; Score 28; DB 2; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 KSTNTFC 13  
 DB :||| |  
 3 RSTNTGC 9  
 RESULT 13  
 AAB10896  
 ID AAB10896 standard; protein; 9 AA.  
 AC AAB10896;  
 XX 26-JAN-2001 (first entry)  
 XX Human 9D7 protein immunogenic fragment SEQ ID NO: 55.  
 XX Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;  
 KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;  
 KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.  
 XX Homo sapiens.  
 OS DE19909503-A1.  
 PN 07-SEP-2000.  
 PD 04-MAR-1999; 99DE-01009503.  
 XX 04-MAR-1999; 99DE-01009503.  
 PR (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
 PA Klade C, Adolf G, Sommergruber W, Heider K;  
 PI WPI; 2000-580357/56.  
 XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer  
 PT and for producing diagnostic or therapeutic antibodies.  
 XX Claim 6; Page 45; 50pp; German.  
 XX This invention describes a novel tumor-associated antigen, designated 9D7  
 CC which has cytostatic activity. The invention also describes a method for  
 CC isolating (a) a polypeptide (I) that includes (S1) as part of its  
 CC sequence; (b) an immunogenic protein fragment or peptide (II) derived  
 CC from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,  
 CC (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a  
 CC protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)  
 CC a recombinant DNA (IIia) that includes (III); and (f) antibodies (Ab)  
 CC directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use  
 CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7  
 CC can be used similarly and cells that express 9D7 are useful in cellular  
 CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for  
 CC imaging, diagnosing and monitoring cancers, also, when conjugated to  
 CC cytotoxins or radionuclide, as therapeutic agents. Peptides derived from  
 CC 9D7 may also be used diagnostically to test for an immune response. 9D7-  
 CC associated cancers are particularly kidney, lung, colon and breast  
 CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic  
 CC fragments of the human tumor-associated antigen 9D7 which is described in  
 CC the method of the invention  
 XX Sequence 9 AA;  
 SQ Query Match 38.9%; Score 28; DB 3; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CASELCK 7  
 DB :||| |  
 3 CGSLGK 9  
 RESULT 14  
 AAE26783  
 ID AAE26783 standard; peptide; 9 AA.  
 XX AAE26783;  
 AC AAE26783;  
 XX 13-DEC-2002 (first entry)  
 XX Fibrin binding peptide #36.  
 DE Fibrin binding peptide; thrombosis; pulmonary embolism; atherosclerosis;  
 KW myocardial infarct; ischaemia; imaging; rheumatoid arthritis; vasotropic;  
 KW anaemia; hypoxia; tumour; diabetic retinopathy; autoimmune disorder;  
 KW inflammatory disorder; angiogenesis; stroke; cerebroprotective.  
 XX Unidentified.  
 OS WO200255544-A2.  
 PN 18-JUL-2002.  
 PD 21-DEC-2001; 2001WO-US049534.  
 XX 23-DEC-2000; 2000US-00747403.  
 PR (DYAX-) DYAX CORP.  
 PA Wescott CR, Beltzer JP, Sato AK;  
 PI WPI; 2002-666875/71.  
 XX Novel synthetic fibrin-binding moiety, useful for detecting, imaging or  
 PT localizing fibrin-containing clots by magnetic resonance imaging,  
 PT radioimaging and for treating diseases involving thrombus formation e.g.  
 PT stroke.  
 XX Claim 4; Page 55; 89pp; English.  
 XX The invention relates to a synthetic fibrin binding group having affinity  
 CC for fibrin. The invention is useful for detecting fibrin in a mammalian  
 CC subject which involves (a) detectably labelling the binding group; (b)  
 CC administering to the subject the labelled polypeptide, and (c) detecting  
 CC the labelled polypeptide in the subject. The invention is useful for  
 CC treating a disease involving thrombus formation eg. deep-vein thrombosis,  
 CC pulmonary embolism, cardiogenic thrombosis, atherosclerosis, myocardial  
 CC infarct, reperfusion ischaemia or stroke. The binding moieties are useful  
 CC for detection, imaging and localisation of fibrin-containing clots by  
 CC magnetic resonance imaging, radioimaging and other imaging methods and  
 CC are also useful in the diagnosis and treatment of coronary conditions  
 CC where fibrin plays a role. The fibrin binding moieties are useful for

CC detecting and diagnosing numerous pathophysiologies in which fibrin plays  
CC a role eg. peritoneal adhesions which often occur after surgery or  
CC inflammatory and neoplastic processes and are comprised of a fibrin  
CC network, fibroblasts, macrophages and new blood vessels; rheumatoid  
CC arthritis, lupus or septic arthritis which often have bits of fibrin  
CC containing tissues called rice bodies in the synovial fluid of their  
CC joints; thrombocytopenic purpura, a type of anaemia in which deposits in  
CC arterioles causes turbulent blood flow resulting in stress and  
CC destruction of red blood cells. The fibrin specific agents can also be  
CC used to detect hypoxia or ischaemia of heart, kidney, liver, lung, brain  
CC or other organs, as well as the detection of tumours, diabetic  
CC retinopathy, early or high-risk atherosclerosis and other autoimmune and  
CC inflammatory disorders. Fibrin specific agents also could provide both  
CC direct or surrogate markers of disease models in which hypoxia and  
CC angiogenesis are expected to play a role. The invention is also useful  
CC for screening molecular libraries. The present sequence is a fibrin  
CC binding peptide  
XX  
SQ Sequence 9 AA;

Query Match 38.9%; Score 28; DB 5; Length 9;  
Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 6 GKSTNTFC 13  
| : : : :  
Db 2 GQESTTFC 9

RESULT 15  
AAB10895  
ID AAB10895 standard; protein; 10 AA.  
XX  
AC AAB10895;  
XX  
DT 26-JAN-2001 (first entry)  
XX  
DE Human 9D7 protein immunogenic fragment SEQ ID NO: 54.  
XX  
KW Tumor-associated antigen; 9D7; human; cytostatic; immunogenic;  
KW immunotherapy; cancer; cellular anticancer vaccine; diagnostic; kidney;  
KW lung; colon; breast; carcinoma; Hodgkin's lymphoma.  
XX  
OS Homo sapiens.  
XX  
XX DE19909503-A1.  
XX  
XX 07-SEP-2000.  
XX  
XX 04-MAR-1999; 99DE-01009503.  
XX  
XX 04-MAR-1999; 99DE-01009503.  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
XX  
XX Klade C, Adolf G, Sommergruber W, Heider K;  
XX  
XX WPI; 2000-588357/56.  
XX  
XX New tumor-associated antigen 9D7, useful e.g. for immunotherapy of cancer  
XX and for producing diagnostic or therapeutic antibodies.  
XX  
XX Claim 6; Page 45; 50pp; German.

XX This invention describes a novel tumor-associated antigen, designated 9D7  
XX which has cytostatic activity. The invention also describes a method for  
XX isolating (a) a polypeptide (I) that includes (S1) as part of its  
XX sequence; (b) an immunogenic protein fragment or peptide (II) derived  
XX from 9D7; (c) a pharmaceutical composition containing at least 1 of 9D7,  
XX (I) or (II) as active ingredients; (d) an isolated DNA (III) encoding a  
XX protein (IV) with the immunogenic properties of 9D7 or its fragments; (e)  
XX a recombinant DNA (IIa) that includes (III); and (f) antibodies (Ab)  
XX directed against 9D7, (I) or (II). 9D7, or its derived immunogenic

CC peptides, are used to induce a humoral and/or cellular response for use  
CC in vivo or ex vivo immunotherapy of cancer. DNA (III) that encodes 9D7  
CC can be used similarly and cells that express 9D7 are useful in cellular  
CC anticancer vaccines. Antibodies (Ab) specific for 9D7 are useful for  
CC imaging, diagnosing and monitoring cancers, also, when conjugated to  
CC cytotoxins or radionuclide, as therapeutic agents. Peptides derived from  
CC 9D7 may also be used diagnostically to test for an immune response. 9D7-  
CC associated cancers are particularly kidney, lung, colon and breast  
CC carcinoma and Hodgkin's lymphoma. AAB10874-B10899 represent immunogenic  
CC fragments of the human tumor-associated antigen 9D7 which is described in  
CC the method of the invention  
XX  
SQ Sequence 10 AA;  
Query Match 38.9%; Score 28; DB 3; Length 10;  
Best Local Similarity 71.4%; Pred. No. 5.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CASELQK 7  
| : : : :  
Db 4 CGSRLQK 10

Search completed: September 5, 2004, 10:30:29  
Job time : 67 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:02 ; Search time 67 Seconds  
(without alignments)  
61.132 Million cell updates/sec

Title: US-09-761-636A-5  
Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 191768

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	69	95.8	13	9 US-09-761-636A-15	Sequence 15, Appl
3	65	90.3	13	9 US-09-761-636A-16	Sequence 16, Appl
4	65	90.3	13	9 US-09-761-636A-18	Sequence 18, Appl
5	61	84.7	13	9 US-09-761-636A-17	Sequence 17, Appl
6	32	44.4	13	16 US-10-415-665-14	Sequence 14, Appl
7	30	41.7	10	14 US-10-208-304-14	Sequence 14, Appl
8	29	40.3	13	16 US-10-415-665-15	Sequence 15, Appl
9	28	38.9	9	14 US-10-034-974-55	Sequence 55, Appl
10	28	38.9	13	16 US-10-415-665-8	Sequence 8, Appl
11	28	38.9	13	16 US-10-415-665-11	Sequence 11, Appl
12	27	37.5	10	10 US-09-572-822C-626	Sequence 626, App
13	27	37.5	10	14 US-10-271-343-19	Sequence 19, Appl
14	27	37.5	12	10 US-09-791-393-262	Sequence 262, App
15	27	37.5	12	10 US-09-791-389-262	Sequence 262, App

16	27	37.5	12	12 US-09-142-613-22	Sequence 22, Appl
17	27	37.5	12	12 US-10-014-340-84	Sequence 84, Appl
18	27	37.5	13	12 US-10-362-527-269	Sequence 269, App
19	27	37.5	13	14 US-10-322-210-67	Sequence 67, Appl
20	27	37.5	13	14 US-10-304-443-67	Sequence 67, Appl
21	27	37.5	13	16 US-10-415-665-10	Sequence 10, Appl
22	27	37.5	13	16 US-10-415-665-12	Sequence 12, Appl
23	27	37.5	13	16 US-10-415-665-13	Sequence 13, Appl
24	26	36.1	8	9 US-09-795-006A-140	Sequence 140, App
25	26	36.1	9	15 US-10-117-937-572	Sequence 572, App
26	26	36.1	9	15 US-10-044-844-70	Sequence 70, Appl
27	26	36.1	10	10 US-09-572-404B-2743	Sequence 2743, App
28	26	36.1	10	10 US-09-572-404B-3191	Sequence 3191, Ap
29	26	36.1	10	10 US-09-572-270A-956	Sequence 956, App
30	26	36.1	10	12 US-10-398-104-128	Sequence 128, App
31	26	36.1	10	14 US-10-208-304-12	Sequence 12, Appl
32	26	36.1	10	14 US-10-208-304-13	Sequence 13, Appl
33	26	36.1	10	14 US-10-208-304-15	Sequence 15, Appl
34	26	36.1	10	14 US-10-208-304-16	Sequence 16, Appl
35	26	36.1	10	15 US-10-117-937-573	Sequence 573, App
36	26	36.1	11	12 US-10-398-104-153	Sequence 153, App
37	26	36.1	11	12 US-10-398-104-268	Sequence 268, App
38	26	36.1	11	16 US-10-415-665-82	Sequence 82, Appl
39	26	36.1	12	12 US-09-142-613-10	Sequence 10, Appl
40	26	36.1	12	16 US-10-415-665-66	Sequence 66, Appl
41	26	36.1	12	16 US-10-415-665-74	Sequence 74, Appl
42	26	36.1	13	10 US-09-792-686A-26	Sequence 26, Appl
43	26	36.1	13	12 US-10-609-217-170	Sequence 170, App
44	26	36.1	13	12 US-10-632-388-170	Sequence 170, App
45	26	36.1	13	12 US-10-651-723-170	Sequence 170, App

## ALIGNMENTS

RESULT 1  
US-09-761-636A-5  
; Sequence 5, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-636A-5

Query Match 100.0%; Score 72; DB 9; Length 13;  
Best Local Similarity 100.0%; Pred. No. 6.6e-06;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CASELGKSTNTFC 13  
Db 1 CASELGKSTNTFC 13

RESULT 2  
US-09-761-636A-15  
; Sequence 15, Application US/09761636A  
; Patent No. US20020065218A1

; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-761-636A-15

Query Match 95.8%; Score 69; DB 9; Length 13;  
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RESULT 3  
US-09-761-636A-16  
; Sequence 16, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
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; LENGTH: 13  
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; ORGANISM: synthetic construct  
US-09-761-636A-16

Query Match 90.3%; Score 65; DB 9; Length 13;  
Best Local Similarity 84.6%; Pred. No. 0.00011;  
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Qy 1 CASELGKSTNTFC 13  
Db 1 CASELGKSTNTFC 13

RESULT 4  
US-09-761-636A-18  
; Sequence 18, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela

; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
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US-09-761-636A-18

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RESULT 5  
US-09-761-636A-17  
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; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
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; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-761-636A-17

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RESULT 6  
US-10-415-665-14  
; Sequence 14, Application US/10415665  
; Publication No. US20040087765A1  
; GENERAL INFORMATION:  
; APPLICANT: Egner, Ralf  
; APPLICANT: Kunze, Rudolf  
; APPLICANT: Winkler, Dirk  
; APPLICANT: Roenspeck, Wolfgang  
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for  
; TITLE OF INVENTION: Binding Immunoglobulins  
; FILE REFERENCE: P68842US0  
; CURRENT APPLICATION NUMBER: US/10/415.665  
; CURRENT FILING DATE: 2003-10-16

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; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
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; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
US-10-415-665-14

Query Match      44.4%; Score 32; DB 16; Length 13;
Best Local Similarity 85.7%; Pred. No. 80;
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QY 1 CASELKGK 7
Db 2 CASHLKG 8

RESULT 7
US-10-208-304-14
; Sequence 14, Application US/10208304
; Publication No. US20030124571A1
; GENERAL INFORMATION:
; APPLICANT: Larisch, Sarit
; APPLICANT: Kim, Seong-Jin
; APPLICANT: Lechleider, Robert J.
; APPLICANT: Roberts, Anita B.
; APPLICANT: Vi, Youngsuk
; TITLE OF INVENTION: NOVEL HUMAN SEPTIN AND USES THEREFOR
; FILE REFERENCE: 11613.42USW1
; CURRENT APPLICATION NUMBER: US/10/208,304
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: PCT/US01/02466
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/178,866
; PRIOR FILING DATE: 2000-01-29
; PRIOR APPLICATION NUMBER: US 60/258,725
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Drosophila
US-10-208-304-14

Query Match      41.7%; Score 30; DB 14; Length 10;
Best Local Similarity 87.5%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ASELGKST 9
Db 2 ASGLGKST 9

RESULT 8
US-10-415-665-15
; Sequence 15, Application US/10415665
; Publication No. US20040087765A1
; GENERAL INFORMATION:
; APPLICANT: Egner, Ralf
; APPLICANT: Kunze, Rudolf
; APPLICANT: Winkler, Dirk
; APPLICANT: Roenspeck, Wolfgang
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; TITLE OF INVENTION: Binding Immunoglobulins

; FILE REFERENCE: P68842US0
; CURRENT APPLICATION NUMBER: US/10/415,665
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/EP01/12933
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: EP00124418.5
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:
; OTHER INFORMATION: synthetic peptide having affinity for
; OTHER INFORMATION: immunoglobulins
US-10-415-665-15

Query Match      40.3%; Score 29; DB 16; Length 13;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELKGK 7
Db 2 CATHLKG 8

RESULT 9
US-10-034-974-55
; Sequence 55, Application US/10034974
; Publication No. US20030143158A1
; GENERAL INFORMATION:
; APPLICANT: DYAX CORP.
; APPLICANT: Beltzer, James P.
; APPLICANT: Wescott, Charles R.
; APPLICANT: Sato, Aaron K.
; TITLE OF INVENTION: FIBRIN BINDING MOIETIES USEFUL AS IMAGING AGENTS
; FILE REFERENCE: DYX-024.1 PCT; DYX-024.1 US
; CURRENT APPLICATION NUMBER: US/10/034,974
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 09/747,403
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fibrin binding polypeptides
US-10-034-974-55

Query Match      38.9%; Score 28; DB 14; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTFC 13
Db 2 QGESRTFC 9

RESULT 10
US-10-415-665-8
; Sequence 8, Application US/10415665
; Publication No. US20040087765A1
; GENERAL INFORMATION:
; APPLICANT: Egner, Ralf
; APPLICANT: Kunze, Rudolf
; APPLICANT: Winkler, Dirk
; APPLICANT: Roenspeck, Wolfgang
; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for
; TITLE OF INVENTION: Binding Immunoglobulins

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; FILE REFERENCE: P68842USO  
; CURRENT APPLICATION NUMBER: US/10/415,665  
; CURRENT FILING DATE: 2003-10-16  
; PRIOR APPLICATION NUMBER: PCT/EP01/12933  
; PRIOR FILING DATE: 2001-11-08  
; PRIOR APPLICATION NUMBER: EP00124418.5  
; PRIOR FILING DATE: 2000-11-08  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial sequence

; OTHER INFORMATION: Description of the artificial sequence:  
; OTHER INFORMATION: synthetic peptide having affinity for  
; OTHER INFORMATION: immunoglobulins  
US-10-415-665-8

Query Match 38.9%; Score 28; DB 16; Length 13;  
Best Local Similarity 71.4%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGK 7  
|||  
Db 2 CAEHLGK 8

RESULT 11  
US-10-415-665-11

; Sequence 11, Application US/10415665  
; Publication No. US20040087765A1

; GENERAL INFORMATION:

; APPLICANT: Egner, Ralf

; APPLICANT: Kunze, Rudolf

; APPLICANT: Winkler, Dirk

; APPLICANT: Roenspeck, Wolfgang

; TITLE OF INVENTION: Peptides, Preparation Thereof and Use Thereof for

; TITLE OF INVENTION: Binding Immunoglobulins

; FILE REFERENCE: P68842USO

; CURRENT APPLICATION NUMBER: US/10/415,665

; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: PCT/EP01/12933

; PRIOR FILING DATE: 2001-11-08

; PRIOR APPLICATION NUMBER: EP00124418.5

; PRIOR FILING DATE: 2000-11-08

; NUMBER OF SEQ ID NOS: 88

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence:

; OTHER INFORMATION: synthetic peptide having affinity for

; OTHER INFORMATION: immunoglobulins

US-10-415-665-11

Query Match 38.9%; Score 28; DB 16; Length 13;  
Best Local Similarity 71.4%; Pred. No. 4.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELKGK 7  
|||  
Db 2 CAEHLGK 8

RESULT 12

US-09-573-822C-626

; Sequence 626, Application US/09573822C

; Publication No. US20030199011A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq  
; FILE REFERENCE: Microbe patent

; CURRENT APPLICATION NUMBER: US/09/573,822C

; CURRENT FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 804

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 626

; LENGTH: 10

; TYPE: PRT

; ORGANISM: mycoplasma genitalium

; FEATURE:

; OTHER INFORMATION: Sequence located in MG309 at 847-856 and may interact with Sequen

; OTHER INFORMATION: in this patent.

US-09-573-822C-626

Query Match 37.5%; Score 27; DB 10; Length 10;  
Best Local Similarity 40.0%; Pred. No. 4.7e+02;  
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 SELGKSTNTF 12  
:|:|:|:|:  
Db 1 AKLSRTTNSF 10

RESULT 13

US-10-271-343-19

; Sequence 19, Application US/10271343

; Publication No. US20030166003A1

; GENERAL INFORMATION:

; APPLICANT: Cochran, Andrea G.

; APPLICANT: Skelton, Nicholas J.

; APPLICANT: Starovashnik, Melissa A.

; TITLE OF INVENTION: A STRUCTURED PEPTIDE SCAFFOLD FOR DISPLAYING TURN LIBRARIES

; TITLE OF INVENTION: ON PHAGE

; FILE REFERENCE: 11669.116US11

; CURRENT APPLICATION NUMBER: US/10/271,343

; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: US 09/592,695

; PRIOR FILING DATE: 2000-06-13

; PRIOR APPLICATION NUMBER: US 60/139,017

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 19

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Turn Peptide

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (3)..(3)

; OTHER INFORMATION: Xaa is independently Trp, Tyr, Leu, Val, or Thr

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (5)..(5)

; OTHER INFORMATION: Xaa is D-pro

US-10-271-343-19

Query Match 37.5%; Score 27; DB 14; Length 10;  
Best Local Similarity 55.6%; Pred. No. 4.7e+02;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELKGKST 9  
|||  
Db 1 CTXEXGKLT 9

RESULT 14

US-09-791-393-262

; Sequence 262, Application US/09791393

; Publication No. US20030032200A1

; GENERAL INFORMATION:



; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N1  
; CURRENT APPLICATION NUMBER: US/09/791,393  
; CURRENT FILING DATE: 2002-01-02  
; EARLIER FILING DATE: 2000-02-24  
; EARLIER APPLICATION NUMBER: GB 0004412.3  
; EARLIER FILING DATE: 2000-02-24  
; EARLIER APPLICATION NUMBER: GB 0030050.9  
; EARLIER FILING DATE: 2000-12-08  
; EARLIER APPLICATION NUMBER: US 60/254,830  
; EARLIER FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 262  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-393-262

Query Match 37.5%; Score 27; DB 10; Length 12;  
Best Local Similarity 57.1%; Pred. No. 5.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CASELKG 7  
Db 6 CTTELGR 12

RESULT 15  
US-09-791-389-262  
; Sequence 262, Application US/09791389  
; Publication No. US20030032773A1  
; GENERAL INFORMATION:  
; APPLICANT: Herath, Herath Mudiyanseelage Athula Chandrasiri  
; APPLICANT: Parekh, Rajesh Bhikhu  
; APPLICANT: Rohlf, Christian  
; APPLICANT: Terrett, Jonathan Alexander  
; APPLICANT: Tyson, Kerry Louise  
; TITLE OF INVENTION: Proteins, Genes and Their Use for  
; TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)  
; TITLE OF INVENTION: and Unipolar Depression  
; FILE REFERENCE: 2543-1-001 N2  
; CURRENT APPLICATION NUMBER: US/09/791,389  
; CURRENT FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: GB 0004412.3  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: GB 0030050.9  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: US 60/254,830  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 308  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 262  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: homo sapien  
US-09-791-389-262

Query Match 37.5%; Score 27; DB 10; Length 12;  
Best Local Similarity 57.1%; Pred. No. 5.7e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 CASELKG 7  
Db 6 CTTELGR 12

Search completed: September 5, 2004, 10:37:18  
Job time : 68 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:29:31 ; Search time 15 Seconds  
(without alignments)  
44.743 Million cell updates/sec

Title: US-09-761-636A-5  
Perfect score: 72  
Sequence: 1 CASELGKSTNTFC 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 127817

Minimum DB seq length: 0  
Maximum DB seq length: 13

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2.6/prodata/2/iaa/5A\_COMB.pep: \*  
2: /cgn2.6/prodata/2/iaa/5B\_COMB.pep: \*  
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5: /cgn2.6/prodata/2/iaa/PCUTUS\_COMB.pep: \*  
6: /cgn2.6/prodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	38.9	9	3	US-09-258-754-63
2	28	38.9	9	3	US-09-042-107-63
3	28	38.9	9	4	US-09-722-250D-63
4	27	37.5	13	1	US-07-732-114A-2
5	27	37.5	13	1	US-08-170-114A-2
6	26	36.1	9	3	US-08-660-092-70
7	26	36.1	9	4	US-09-160-513-70
8	26	36.1	13	3	US-09-258-754-219
9	26	36.1	13	3	US-09-042-107-219
10	26	36.1	13	4	US-09-722-250D-219
11	26	36.1	13	4	US-09-428-082B-170
12	24.5	34.0	12	4	US-08-182-967-12
13	24	33.3	7	2	US-08-645-193B-3
14	24	33.3	9	6	5217869-110
15	24	33.3	11	3	US-08-866-545-24
16	24	33.3	11	4	US-09-428-082B-116
17	24	33.3	11	4	US-09-627-775-24
18	24	33.3	13	3	US-09-258-754-183
19	24	33.3	13	3	US-09-042-107-183
20	24	33.3	13	4	US-08-182-967-11
21	24	33.3	13	4	US-07-732-250D-183
22	23.5	32.6	11	1	US-07-732-114A-6
23	23.5	32.6	11	1	US-08-170-114A-6
24	23	31.9	7	2	US-08-645-193B-7
25	23	31.9	7	2	US-08-645-193B-59
26	23	31.9	9	3	US-08-660-092-150
27	23	31.9	9	3	US-08-660-092-151

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28 23 31.9 9 3 US-08-660-092-152 Sequence 152, Appl
29 23 31.9 9 4 US-09-160-513-150 Sequence 150, Appl
30 23 31.9 9 4 US-09-160-513-151 Sequence 151, Appl
31 23 31.9 9 4 US-09-160-513-152 Sequence 152, Appl
32 23 31.9 10 1 US-08-250-789A-91 Sequence 91, Appl
33 23 31.9 10 4 US-09-489-847-344 Sequence 344, Appl
34 23 31.9 11 1 US-08-212-433A-30 Sequence 30, Appl
35 23 31.9 11 3 US-08-716-256-30 Sequence 30, Appl
36 23 31.9 11 4 US-09-069-827A-35 Sequence 35, Appl
37 23 31.9 11 5 PCT-US95-03239-30 Sequence 30, Appl
38 23 31.9 12 1 US-07-732-114A-1 Sequence 1, Appl
39 23 31.9 12 1 US-08-170-114A-1 Sequence 1, Appl
40 23 31.9 12 4 US-08-811-682-20 Sequence 20, Appl
41 23 31.9 12 4 US-09-089-878-1 Sequence 1, Appl
42 23 31.9 13 4 US-09-089-878-2 Sequence 1, Appl
43 22.5 31.2 12 4 US-09-460-384-9 Sequence 2, Appl
44 22 30.6 7 4 US-09-187-859-1066 Sequence 9, Appl
45 22 30.6 7 4 US-09-839-542B-1066 Sequence 1066, Ap

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## ALIGNMENTS

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RESULT 1
US-09-258-754-63
; Sequence 63, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; US-09-258-754-63

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Query Match          38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 7 KSTNTFC 13
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Db 3 RSTNTGC 9

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RESULT 2
US-09-042-107-63
; Sequence 63, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-63

Query Match          38.9%; Score 28; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

QY      7 KSTNTFC 13
       :|||||
Db      3 RSTNTGC 9

RESULT 3
US-09-722-250D-63
; Sequence 63, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-63

Query Match          38.9%; Score 28; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 1;

QY      7 KSTNTFC 13
       :|||||
Db      3 RSTNTGC 9

RESULT 4
US-07-732-114A-2
; Sequence 2, Application US/07732114A
; Patent No. 5298396
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Beaton & Swanson, P.C.
; STREET: 4582 South Ulster Street Parkway, #403
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80237
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NUH217.3
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; APPLICATION NUMBER: US/07/732,114A
; FILING DATE: 18-JULY-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 850-9900
; TELEFAX: (303) 850-9401
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-07-732-114A-2

Query Match          37.5%; Score 27; DB 1; Length 13;
Best Local Similarity 54.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CASELGKSTNT 11
       :|||
Db      1 CASSLYGTRNT 11

RESULT 5
US-08-170-114A-2
; Sequence 2, Application US/08170114A
; Patent No. 5776708
; GENERAL INFORMATION:
; APPLICANT: KOTZIN, BRIAN L.
; APPLICANT: MARRACK, PHILIPPA
; APPLICANT: KAPPLER, JOHN
; APPLICANT: PALLARD, XAVIER
; TITLE OF INVENTION: METHOD FOR IDENTIFYING T CELLS
; TITLE OF INVENTION: INVOLVED IN AUTOIMMUNE DISEASE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0 (a) For Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/170,114A
; FILING DATE: 20-DECEMBER-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/732,114
; FILING DATE: 18-JULY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,488,353
; FILING DATE: 2-MARCH-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07,437,370
; FILING DATE: 15-NOVEMBER-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Julie L. Bernard
; REGISTRATION NUMBER: 36,450
; REFERENCE/DOCKET NUMBER: NUH217.3
```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 13 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-170-114A-2

Query Match 37.5%; Score 27; DB 1; Length 13;  
Best Local Similarity 54.5%; Pred. No. 2.le+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTNT 11  
DB 1 CASSLYGTRNT 11

## RESULT 6

US-08-660-092-70  
Sequence 70, Application US/08660092  
Patent No. 6207160  
GENERAL INFORMATION:  
APPLICANT: Victoria, Edward J.  
APPLICANT: Marquis, David M.  
APPLICANT: Jones, David S.  
APPLICANT: Yu, Lin  
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES  
TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR aPL ANTIBODY-MEDIATED  
TITLE OF INVENTION: PATHOLOGIES  
NUMBER OF SEQUENCES: 216  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/660,092  
FILING DATE: 06-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Park, Freddie K.  
REGISTRATION NUMBER: 35,636  
REFERENCE/DOCKET NUMBER: 25231-20061.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-660-092-70

Query Match 36.1%; Score 26; DB 3; Length 9;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7  
DB 1 CAGVLGK 7

## RESULT 7

US-09-160-513-70  
Sequence 70, Application US/09160513  
Patent No. 6410775  
GENERAL INFORMATION:  
APPLICANT: Victoria, Edward J.  
APPLICANT: Marquis, David M.  
APPLICANT: Jones, David S.  
APPLICANT: Yu, Lin  
TITLE OF INVENTION: aPL IMMUNOREACTIVE PEPTIDES, CONJUGATES THEREOF AND METHODS O  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/160,513  
FILING DATE: 1998-DEC-24  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CATHERINE M. POLIZZI  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 25231-20061.01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 813-5600  
TELEFAX: (650) 494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-160-513-70

Query Match 36.1%; Score 26; DB 4; Length 9;  
Best Local Similarity 71.4%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGK 7  
DB 1 CAGVLGK 7

## RESULT 8

US-09-258-754-219  
Sequence 219, Application US/09258754  
Patent No. 6174687  
GENERAL INFORMATION:  
APPLICANT: Ruoslahti, Erkki  
APPLICANT: Pasqualini, Renata  
APPLICANT: Rajotte, Daniel  
TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
TITLE OF INVENTION: Membrane Dipeptidase  
FILE REFERENCE: P-LJ 3443  
CURRENT APPLICATION NUMBER: US/09/258,754  
CURRENT FILING DATE: 1999-02-26  
EARLIER APPLICATION NUMBER: 09/042,107  
EARLIER FILING DATE: 1998-03-13  
NUMBER OF SEQ ID NOS: 452  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 219  
LENGTH: 13

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-219

Query Match      36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 9
US-09-042-107-219
; Sequence 219, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-219

Query Match      36.1%; Score 26; DB 3; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 10
US-09-722-250D-219
; Sequence 219, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-219

Query Match      36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 30.8%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 7; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CGSHCGQLCKSLC 13

RESULT 11
US-09-428-082B-170
; Sequence 170, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428,082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 170
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CALMODULIN ANTAGONIST PEPTIDE
US-09-428-082B-170

Query Match      36.1%; Score 26; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NTFC 13
Db 8 NTFC 11

RESULT 12
US-08-182-967-12
; Sequence 12, Application US/08182967
; Patent No. 6413516
; GENERAL INFORMATION:
; APPLICANT: Chang, Jennie C.C.
; APPLICANT: Brostoff, Steven W.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Peptides and Methods Against Psoriasis
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/182,967
; FILING DATE: 14-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,471
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/813,867
; FILING DATE: 14-DEC-1991
; PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 07/644,611
/ FILING DATE: 22-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/530,229
/ FILING DATE: 30-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,085
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,086
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/326,314
/ FILING DATE: 21-MAR-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-IM 9830
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-182-967-12

Query Match 34.0%; Score 24.5; DB 4; Length 12;
Best Local Similarity 63.6%; Pred. No. 5e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11
DB 1 CASSL-NSLNT 10

RESULT 13
US-08-645-193B-3
/ Sequence 3, Application US/08645193B
/ Patent No. 5962253
/ GENERAL INFORMATION:
/ APPLICANT: Kupke, Thomas
/ APPLICANT: Gotz, Friedrich
/ APPLICANT: Kempster, Christoph
/ APPLICANT: Jung, Gunther
/ TITLE OF INVENTION: Oxidative Decarboxylation of Peptides
/ TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
/ NUMBER OF SEQUENCES: 70
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
/ STREET: 1100 New York Avenue, Suite 600
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/645,193B
/ FILING DATE: 13-MAY-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Esmond, Robert W.
/ REGISTRATION NUMBER: 32,893
/ REFERENCE/DOCKET NUMBER: 0652.1540000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 371-2600
/ TELEFAX: (202) 371-2540

/ APPLICATION NUMBER: US 07/644,611
/ FILING DATE: 22-JAN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/530,229
/ FILING DATE: 30-MAY-1990
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,085
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/382,086
/ FILING DATE: 18-JUL-1989
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/326,314
/ FILING DATE: 21-MAR-1989
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-IM 9830
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 7 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: single
/ MOLECULE TYPE: peptide
/ US-08-645-193B-3

Query Match 33.3%; Score 24; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 STNTFC 13
DB 1 SFNSFC 6

RESULT 14
5217869-110
/ Patent No. 5217869
/ APPLICANT: KAUVAR, LAWRENCE M.
/ TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
/ REAGENTS
/ NUMBER OF SEQUENCES: 121
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/255,906
/ FILING DATE: 11-OCT-1988
/ SEQ ID NO: 110:
/ LENGTH: 9
/ 5217869-110

Query Match 33.3%; Score 24; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GKSTNTF 12
DB 1 KGGSNNF 7

RESULT 15
US-08-866-545-24
/ Sequence 24, Application US/08866545
/ Patent No. 6265535
/ GENERAL INFORMATION:
/ APPLICANT: Greene, Mark I.
/ APPLICANT: Murali, Ramachandran
/ APPLICANT: Takasaki, Wataru
/ TITLE OF INVENTION: PEPTIDES AND PEPTIDE
/ TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
/ TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
/ TITLE OF INVENTION: USES
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2811
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/866,545
/ FILING DATE: 30-MAY-1997
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
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ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 009113-0004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-493-4935  
TELEFAX: 650-493-5556  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: NO. 6265535e  
US-08-866-545-24

Query Match 33.3%; Score 24; DB 3; Length 11;  
Best Local Similarity 57.1%; Pred. No. 5.6e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CASELCK 7  
Db 2 CRKELGQ 8

Search completed: September 5, 2004, 10:32:42  
Job time : 16 secs



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:36:12 ; Search time 22 Seconds

(without alignments)  
34.979 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 605

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	37.0	6	2	S29637	Jacalin beta-II chain
2	17	37.0	6	2	I37263	Y protein - human (fragment)
3	15	32.6	6	2	JU0355	Lipopeptide WS1279
4	15	32.6	7	2	B39040	Calasestrin, fas
5	15	32.6	8	2	S59622	Metallothionein is
6	15	32.6	8	2	S13288	Acylase - Kluyvera
7	15	32.6	8	2	S63165	Ferredoxin a2 - Ja
8	14	30.4	6	2	B31263	Dihydrofolate redu
9	14	30.4	6	2	S29881	Na+/K+-exchanging
10	14	30.4	7	1	XEYDGD	Galactose oxidase
11	14	30.4	8	2	B47594	Aspartate kinase (
12	13	28.3	5	2	A32014	Tram protein - Esc
13	13	28.3	8	2	A37521	R-phycoerythrin ga
14	12	26.1	6	2	H48394	Glycoprotein compo
15	12	26.1	7	2	B34818	Vicilin 57K chain
16	12	26.1	7	2	A12016	Formylglycinamide
17	12	26.1	8	2	PC1002	Leucine-tRNA ligase
18	11	23.9	4	2	A41890	Protein D - Echer
19	11	23.9	5	2	A26830	Mitosis inhibiting
20	11	23.9	5	2	B25655	R-phycoerythrin al
21	11	23.9	5	2	A44692	Fulicin - giant Af
22	11	23.9	6	2	A31263	Dihydrofolate redu
23	11	23.9	7	2	A58512	Venom heptapeptide
24	11	23.9	7	2	I46868	Alpha-myosin heavy
25	11	23.9	8	2	C63512	Variant surface gl
26	11	23.9	8	2	PT0554	T-cell receptor be
27	10	21.7	4	2	S55238	Pallidipin - assas
28	10	21.7	5	2	A60803	Neuropeptide - sea
29	10	21.7	5	2	PT0610	T-cell receptor be

## ALIGNMENTS

### RESULT 1

S29637  
Jacalin beta-II chain - Artocarpus champeden (fragment)  
C:Species: Artocarpus champeden  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 24-Jul-1998  
C:Accession: S29637  
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.  
Biochim. Biophys. Acta 1156, 219-222, 1993  
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD  
A:Reference number: S29635; MUID:93152601; PMID:8427879  
A:Accession: S29637  
A:Molecule type: protein  
A:Residues: 1-6 <NGO>  
A:Experimental source: seed  
C:Complex: heterotetramer; two alpha and two beta chains  
C:Function:  
A:Description: seed storage protein  
A>Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine  
C:Keywords: heterotetramer; lectin; seed; storage protein

Query Match 37.0%; Score 17; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	2 NEES 5
DB	1 NEQS 4

### RESULT 2

I37263  
Y protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 12-Aug-1995 #sequence\_revision 12-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I37263  
R:Waechter, G.; Habener, J.F.  
Endocrinology 131, 2010-2015, 1992  
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alterna  
A:Reference number: I37263; MUID:93010691; PMID:1396344  
A:Accession: I37263  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
C:Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816  
C:Genetics:  
A:Gene: CREB

Query Match 37.0%; Score 17; DB 2; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	5 SLIC 8
----	----------

Db |||  
1 SLFC 4

Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# RESULT 3

JU0355  
lipopeptide WS1279 [validated] - Streptomyces willmorei  
C:Species: Streptomyces willmorei  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: JU0355  
R;Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
Chem. Pharm. Bull. 39, 607-611, 1991  
A;Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
A;Reference number: JU0355; MUID:91300586; PMID:2070441  
A;Accession: JU0355  
A;Molecule type: protein  
A;Residues: 1-6 <TSU>  
A;Note: the structure was confirmed by synthesis  
C;Keywords: blocked amino end; lipoprotein  
F;1/Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F;1/Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 32.6%; Score 15; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2  
|||  
Db 1 CN 2

# RESULT 4

B39040  
calsequestrin, fast skeletal muscle - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997  
C:Accession: B39040  
R;Calal, S.E.; Jones, L.R.  
J. Biol. Chem. 266, 391-398, 1991  
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein kinase II  
A;Reference number: A39040; MUID:9109153; PMID:1985907  
A;Accession: B39040  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <CAL>  
C;Keywords: phosphoprotein; skeletal muscle

Query Match 32.6%; Score 15; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6  
: |||  
Db 2 DEEDL 6

# RESULT 5

S59622  
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (fragment)  
C:Species: Ariantha arbustorum  
C>Date: 19-Mar-1997 #sequence\_revision 24-Oct-1997 #text\_change 07-May-1999  
C:Accession: S59622  
R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallingier, R.  
Biochem. J. 311, 951-957, 1995  
A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothionein isoforms from the terrestrial snail Ariantha arbustorum  
A;Reference number: S59621; MUID:96067616; PMID:7487956  
A;Accession: S59622  
A;Molecule type: protein  
A;Residues: 1-8 <BER>  
C;Superfamily: metallothionein  
C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 32.6%; Score 15; DB 2; Length 8;

# RESULT 6

S19288  
acylase - Kluyvera cryocrescens  
C:Species: Kluyvera cryocrescens  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997  
C:Accession: S19288  
R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.  
Biochem. J. 280, 659-662, 1991  
A;Title: Chemical modification of serine at the active site of penicillin acylase from Kluyvera cryocrescens  
A;Reference number: S19288; MUID:92109664; PMID:1764029  
A;Accession: S19288  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <MAR>

Query Match 32.6%; Score 15; DB 2; Length 8;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2  
|||  
Db 1 CN 2

# RESULT 7

S69165  
ferredoxin a2 - Japanese radish (fragment)  
C:Species: Kaiware daikon (Japanese radish)  
C>Date: 10-Mar-1998 #sequence\_revision 10-Mar-1998 #text\_change 17-Apr-1998  
C:Accession: S69165  
R;Obata, S.; Nishimura, M.; Nagai, K.; Sakihama, N.; Shin, M.  
Arch. Biochem. Biophys. 316, 797-802, 1995  
A;Title: Four ferredoxins from Japanese radish leaves.  
A;Reference number: S69164; MUID:95168867; PMID:7864635  
A;Accession: S69165  
A;Molecule type: protein  
A;Residues: 1-8 <ORA>  
C;Keywords: 2Fe-2S; electron transfer; iron-sulfur protein

Query Match 32.6%; Score 15; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EESLI 7  
||| :  
Db 4 EEDIV 8

# RESULT 8

B31263  
dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum  
C:Species: Plasmodium falciparum  
C>Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Mar-1996  
C:Accession: B31263  
R;Peterson, D.S.; Walliker, D.; Wellem, T.E.  
Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988  
A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase gene of Plasmodium falciparum confers resistance to pyrimethamine  
A;Reference number: A9421; MUID:89057886; PMID:2904149  
A;Accession: B31263  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-6 <PET>  
C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 30.4%; Score 14; DB 2; Length 6;

Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEESL 6  
DB 2 NWESL 6

RESULT 9  
S29881  
Na+/K+-exchanging ATPase (EC 3.6.3.9) alpha chain - dog (fragment)  
C:Species: Canis lupus familiaris (dog)  
C:Date: 19-Mar-1997 #sequence\_revision 24-Jul-1998 #text\_change 19-Apr-2002  
C:Accession: S29881  
R:Walderhaug, M.O.; Post, R.L.; Saccomani, G.; Leonard, R.T.; Brikin, D.P.  
J. Biol. Chem. 260, 3852-3859, 1985  
A:Title: Structural relatedness of three ion-transport adenosine triphosphatases around  
A:Reference number: S29881; MUID:85131201; PMID:3156136  
A:Accession: S29881  
A:Molecule type: protein  
A:Residues: 1-6 <WAL>  
A:Experimental source: kidney  
C:Keywords: ATP; heterodimer; hydrolase; ion transport; osmoregulation; phosphoprotein;  
F4/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 30.4%; Score 14; DB 2; Length 6;  
Best Local Similarity 20.0%; Pred. No. 2.8e+05;  
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEES 5  
DB 2 CSDST 6

RESULT 10  
XEYDGS  
galactose oxidase inhibitor - fungus (Cladobotryum dendroides)  
C:Species: Cladobotryum dendroides  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 31-Dec-1993  
C:Accession: A01341  
R:Avigad, G.; Markus, Z.  
Fed. Proc. 31, 447, 1972  
A:Reference number: A01341  
A:Accession: A01341  
A:Molecule type: protein  
A:Residues: 1-7 <AVI>  
C:Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxidase, may inactivate the enzyme by binding to its prosthetic copper group.  
C:Superfamily: galactose oxidase inhibitor  
C:Keywords: copper

Query Match 30.4%; Score 14; DB 1; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5  
DB 4 NTES 7

RESULT 11  
B47594  
aspartate kinase (EC 2.7.2.4) beta chain - Corynebacterium flavum (strain N13) (fragment)  
C:Species: Corynebacterium flavum  
C:Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 19-Dec-1997  
C:Accession: B47594  
R:Follettie, M.T.; Peoples, O.P.; Agoropoulou, C.; Sinskey, A.J.  
J. Bacteriol. 175, 4096-4103, 1993  
A:Title: Gene structure and expression of the Corynebacterium flavum N13 ask-asd operon.  
A:Reference number: A47594; MUID:93308089; PMID:8100567  
A:Accession: B47594  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA

A:Residues: 1-8 <FOL>  
C:Keywords: phosphotransferase

Query Match 30.4%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 BESLI 7  
DB 2 BEAVL 6

RESULT 12  
A32014  
traM protein - Escherichia coli plasmid R100 (fragment)  
C:Species: Escherichia coli  
C:Date: 22-Jun-1989 #sequence\_revision 22-Jun-1989 #text\_change 16-Feb-1997  
C:Accession: A32014  
R:Inamoto, S.; Yoshioka, Y.; Ohtsubo, E.  
J. Bacteriol. 170, 2749-2757, 1988  
A:Title: Identification and characterization of the products from the traJ and traY gene  
A:Reference number: A32014; MUID:89227859; PMID:2836369  
A:Accession: A32014  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-5 <INA>  
C:Genetics:  
A:Genome: plasmid  
C:Keywords: DNA binding

Query Match 28.3%; Score 13; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NEE 4  
DB 2 NDE 4

RESULT 13  
A37521  
R-phycoerythrin gamma-E chain - red alga (Gastrocloonium coulteri) (fragment)  
C:Species: Gastrocloonium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: A37521; J22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: A37521  
A:Molecule type: protein  
A:Residues: 1-8 <KLO>

Query Match 28.3%; Score 13; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SLIC 8  
DB 4 ALAC 7

RESULT 14  
H48394  
glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (fr  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 07-Feb-1997  
C:Accession: H48394  
R:Mather, I.H.; Banghart, L.R.; Lane, W.S.  
Biochem. Mol. Biol. Int. 29, 545-554, 1993  
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig  
II-like sequences.  
A:Reference number: A48394; MUID:93250576; PMID:8485470

A;Accession: H48394  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-6 <MA>  
A;Experimental source: milk  
A;Note: sequence extracted from NCBI backbone (NCBIP:131518)  
C;Keywords: glycoprotein

Query Match 26.1%; Score 12; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 ESLIC 8  
DB 2 ELLGC 6

RESULT 15  
B34818  
vicilin 57K chain - pigeon pea (fragment)  
C;Species: Cajanus cajan (pigeon pea)  
C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C;Accession: B34818  
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.  
A;Reference number: A34818; MUID:90165956; PMID:2306256  
A;Accession: B34818  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <MA>

Query Match 26.1%; Score 12; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNE 3  
DB 3 CME 5

Search completed: September 5, 2004, 10:40:20  
Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:47 ; Search time 15 Seconds  
(without alignments)  
27.771 Million cell updates/sec

Title: US-09-761-636A-6  
Perfect score: 46  
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 158

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	14	30.4	7	1	IGAO_DACDE
2	13	28.3	5	1	TRM3_ECOLI
3	13	28.3	7	1	PLP_BRANA
4	12	26.1	7	1	UF03_MOUSE
5	12	26.1	8	1	UPA1_HUMAN
6	11	23.9	7	1	BRHP_CONIM
7	11	23.9	7	1	FAR1_ASCSU
8	11	23.9	8	1	CAD1_ENTFA
9	10	21.7	8	1	ACT_CARMA
10	9	19.6	6	1	TMOF_SARBU
11	9	19.6	8	1	COM2_CONPU
12	9	19.6	8	1	GLUR_HUMAN
13	8	17.4	6	1	ACPH_RABIT
14	8	17.4	6	1	ASP2_LACSN
15	8	17.4	7	1	CCF1_ENTFA
16	8	17.4	7	1	FAR1_PROCL
17	8	17.4	7	1	GRFP_MOUSE
18	8	17.4	7	1	WWA1_ACHFU
19	8	17.4	7	1	WWA3_ACHFU
20	8	17.4	8	1	FAR4_HOMAM
21	8	17.4	8	1	FAR8_CALVO
22	7	15.2	7	1	FAR2_ASCSU
23	7	15.2	7	1	UH11_RAT
24	7	15.2	8	1	CLP_THICU
25	7	15.2	8	1	CPD1_ENTFA
26	7	15.2	8	1	PPK3_PERAM
27	7	15.2	8	1	UH09_RAT
28	7	15.2	8	1	WPI_PERAT
29	6	13.0	4	1	EOST_HUMAN
30	6	13.0	4	1	FLRN_ANFEL
31	6	13.0	5	1	TPIS_CANFA
32	6	13.0	5	1	UXA4_CHLTR
33	6	13.0	6	1	FARP_MONEX

34	6	13.0	6	1	UN06_CLOPA
35	6	13.0	6	1	VP19_HSVIK
36	6	13.0	7	1	ALL2_CARMA
37	6	13.0	7	1	ALL5_CARMA
38	6	13.0	7	1	CHOX_ALCSP
39	6	13.0	7	1	EIO5_LITRU
40	6	13.0	7	1	FAR1_MACRS
41	6	13.0	7	1	FAR2_PROCL
42	6	13.0	7	1	FAR4_PANRE
43	6	13.0	7	1	FARB_CALVO
44	6	13.0	7	1	LANC_CARUI
45	6	13.0	7	1	MNP1_LEPDE

P81351	clostridium
P23210	herpes simp
P81805	carcinus ma
P81808	carcinus ma
P16101	alcaligenes
P82101	litoria rub
P83274	macrobrachi
P38498	procamburus
P41875	panagrellus
P41866	calliphora
P36960	carnobacter
P42984	leptinotars

## ALIGNMENTS

RESULT 1  
IGAO\_DACDE STANDARD; PRT; 7 AA.  
AC P06294;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Galactose oxidase inhibitor  
OS Dactylium dendroides (Cladobotryum dendroides).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
OX NCBI\_TaxID=5132;  
RN [1]  
RP SEQUENCE.  
RA Avigad G., Markus Z.;  
RT "Identification of a peptide inhibitor of galactose oxidase from  
RT Dactylium dendroides.";  
RL Fed. Proc. 31:447-447(1972).  
CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the  
CC galactose oxidase apoenzyme. It may inactivate the enzyme by  
CC binding to its prosthetic copper group.  
DR PIR; A01341; XEYDGD.  
KW Copper; Metalloenzyme inhibitor.  
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NEES 5  
Db 4 NTES 7

RESULT 2  
TRM3\_ECOLI STANDARD; PRT; 5 AA.  
ID TRM3\_ECOLI  
AC P13973;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE TrmM protein (Fragment).  
GN TRAM.  
OS Escherichia coli.  
OG Plasmid IncFII R100.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88227859; PubMed=2836369;  
RA Inamoto S., Yoshioka Y., Ohtsubo E.;  
RT "Identification and characterization of the products from the traj  
RT and trm genes of plasmid R100.";  
RL J. Bacteriol. 170:2749-2757(1988).

CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION

```

CC      PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC      -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -|- SIMILARITY: Belongs to the trm family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
CC      EMBL; M20941; -; NOT_ANNOTATED_CDS.
CC      DR      PIR; A32014; A32014.
CC      KW      Conjugation; Plasmid; DNA-binding.
CC      FT      NON_TER 1
CC      SQ      SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;
CC
CC      Query Match      28.3%; Score 13; DB 1; Length 5;
CC      Best Local Similarity 66.7%; Pred. No. 1.4e+05;
CC      Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY      2 NEE 4
CC      Db      2 NDE 4
CC
CC      RESULT 3
CC      PLP BRANA
CC      ID      PLP BRANA STANDARD; PRT; 8 AA.
CC      AC      P81707;
CC      DT      15-JUL-1999 (Rel. 38, Created)
CC      DT      15-JUL-1999 (Rel. 38, Last sequence update)
CC      DT      30-MAY-2000 (Rel. 39, Last annotation update)
CC      DE      Plastidial lipid-associated protein (Fragment).
CC      OS      Brassica napus (Rape).
CC      OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC      OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
CC      OC      eurosids II; Brassicales; Brassicaceae; Brassica.
CC      OX      NCBI_TaxID=3708;
CC      RN      [1]
CC      RP      SEQUENCE.
CC      RC      STRAIN=CV. TOPAZ; TISSUE=Tapetum;
CC      RX      MEDLINE=99349136; PubMed=10420651;
CC      RA      Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
CC      RA      Murphy D.J.;
CC      RT      "Composition and role of tapetal lipid bodies in the biogenesis of the
CC      RT      pollen coat of Brassica napus.";
CC      RL      Planta 208:588-598(1999).
CC      CC      -|- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC      CC      specific plastidial lipid organelle.
CC      CC      -|- TISSUE SPECIFICITY: Tapetum of anthers.
CC      FT      NON_TER 8
CC      SQ      SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;
CC
CC      Query Match      28.3%; Score 13; DB 1; Length 8;
CC      Best Local Similarity 66.7%; Pred. No. 1.4e+05;
CC      Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC      QY      2 NEE 4
CC      Db      5 NDE 7
CC
CC      RESULT 4
CC      UF03 MOUSE
CC      ID      UF03 MOUSE STANDARD; PRT; 7 AA.
CC      AC      P38641;
CC      DT      01-OCT-1994 (Rel. 30, Created)
CC      DT      01-OCT-1994 (Rel. 30, Last sequence update)
CC      DT      15-MAR-2004 (Rel. 43, Last annotation update)
CC      DE      Unknown protein from 2D-page of fibroblasts (p36) (Fragment).
CC      OS      Mus musculus (Mouse).

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OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC      NCBF_TaxID=10090;
OC      RN      [1]
OC      RP      SEQUENCE.
OC      RC      TISSUE=Fibroblast;
OC      RX      MEDLINE=95009907; PubMed=7523108;
OC      RA      Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
OC      RT      "Separation and sequencing of familial and novel murine proteins
OC      RT      using preparative two-dimensional gel electrophoresis.";
OC      RL      Electrophoresis 15:735-745(1994).
OC      CC      -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
OC      CC      protein is: 5.1, its MW is: 36 kDa.
OC      FT      NON_TER 7
OC      SQ      SEQUENCE 7 AA; 842 MW; 6AA72B1DDDB1B1180 CRC64;
OC
OC      Query Match      26.1%; Score 12; DB 1; Length 7;
OC      Best Local Similarity 50.0%; Pred. No. 1.4e+05;
OC      Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OC
OC      QY      2 NEE 5
OC      Db      1 HEEA 4
OC
OC      RESULT 5
OC      UPAL HUMAN
OC      ID      UPAL HUMAN STANDARD; PRT; 8 AA.
OC      AC      P30087;
OC      DT      01-APR-1993 (Rel. 25, Created)
OC      DT      01-APR-1993 (Rel. 25, Last sequence update)
OC      DT      15-MAR-2004 (Rel. 43, Last annotation update)
OC      DE      Unknown protein from 2D-page of plasma (Spot 2) (Fragment).
OC      OS      Homo sapiens (Human).
OC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC      OX      NCBI_TaxID=9606;
OC      RN      [1]
OC      RP      SEQUENCE.
OC      RC      TISSUE=Plasma;
OC      RX      MEDLINE=93092937; PubMed=1459097;
OC      RA      Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
OC      RA      Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
OC      RA      Hochstrasser D.F.;
OC      RT      "Plasma protein map: an update by microsequencing.";
OC      RL      Electrophoresis 13:707-714(1992).
OC      CC      -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
OC      CC      protein is: 4.9, its MW is: 65 kDa.
OC      CC      SWISS-2DPAGE; P30087; HUMAN.
OC      DR      NON_TER 1
OC      FT      UNSURE 8
OC      FT      NON_TER 8
OC      SQ      SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;
OC
OC      Query Match      26.1%; Score 12; DB 1; Length 8;
OC      Best Local Similarity 50.0%; Pred. No. 1.4e+05;
OC      Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OC
OC      QY      2 NEE 5
OC      Db      1 DQES 4
OC
OC      RESULT 6
OC      BRHP CONIM
OC      ID      BRHP CONIM STANDARD; PRT; 7 AA.
OC      AC      P58803;
OC      DT      28-FEB-2003 (Rel. 41, Created)
OC      DT      28-FEB-2003 (Rel. 41, Last sequence update)
OC      DT      28-FEB-2003 (Rel. 41, Last annotation update)
OC      DE      Bromheptapeptide Im.
OC      OS      Conus imperialis (imperial cone).
OC      OC      Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

```

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=35631;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=97184108; PubMed=9030520;  
 RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,  
 RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,  
 RA McIntosh J.M.;  
 RT "A novel post-translational modification involving bromination of  
 RT tryptophan. Identification of the residue, L-6-bromotryptophan, in  
 RT peptides from *Conus imperialis* and *Conus radiatus* venom.";  
 RL J. Biol. Chem. 272:4689-4698(1997).  
 CC -!- FUNCTION: Does not elicit gross behavioral symptoms when injected  
 CC centrally or peripherally in mice.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=853.19; METHOD=LSIMS.  
 DR PIR; A58512; A58512.  
 KW Bromination; Amidation; Pyrrolidone carboxylic acid.  
 FT DISULFID 2 7  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 6 6 BROMINATION.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
 Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNE 3  
 Db 2 CQ 4

RESULT 7  
 FARI ASCSU  
 ID FARI ASCSU STANDARD; PRT; 7 AA.  
 AC P31869;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE FMRPamide-like neuropeptide AFI.  
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=90180465; PubMed=2627377;  
 RA Cowden C., Stretton A.O.W., Davis R.E.;  
 RT "AFI, a sequenced bioactive neuropeptide isolated from the nematode  
 RT *Ascaris suum*.";  
 RL Neuron 2:1465-1473(1989).  
 CC -!- FUNCTION: Potent modulator of inhibitory motoneurons. Reduces the  
 CC input resistance and blocks slow oscillatory potentials in these  
 CC cells.  
 CC -!- TISSUE SPECIFICITY: Found in the nerve cords and a variety of  
 CC ganglia particularly in the anterior regions.  
 CC -!- SIMILARITY: Belongs to the FARP (FMRPamide related peptide)  
 CC family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 7 7 AMIDATION.  
 SQ SEQUENCE 7 AA; 953 MW; 69D40059CBI44350 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NE 3  
 Db 2 NE 3

RESULT 8  
 CADI\_ENTFA  
 ID CADI\_ENTFA STANDARD; PRT; 8 AA.  
 AC P13268;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-FEB-1991 (Rel. 17, Last annotation update)  
 DE Sex pheromone CADI.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85051889; PubMed=6437872;  
 RA Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,  
 RA Craig R.A., Clewell D.B., Suzuki A.;  
 RT "Isolation and structure of the bacterial sex pheromone, CADI, that  
 RT induces plasmid transfer in *Streptococcus faecalis*.";  
 RL FEBS Lett. 178:97-100(1984).  
 CC -!- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
 CC HEMOLYSIN PLASMID PAD1.  
 KW Pheromone.  
 SQ SEQUENCE 8 AA; 819 MW; 047DD732C735B9C7 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLI 7  
 Db 3 SLV 5

RESULT 9  
 ACT\_CARMA  
 ID ACT\_CARMA STANDARD; PRT; 8 AA.  
 AC P80709;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Actin (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Bagdasarian D.;  
 RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
 RL Endocrine 5:23-32(1996).  
 CC -!- FUNCTION: Actins are highly conserved proteins that are involved  
 CC in various types of cell motility and are ubiquitously expressed  
 CC in all eukaryotic cells.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 6.8, ITS MW IS: 46 kDa.  
 CC -!- SIMILARITY: Belongs to the actin family.  
 DR InterPro; IPR004001; Actin.  
 DR InterPro; IPR004000; Actin.  
 DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE; PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
 KW Structural protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;

Query Match 21.7%; Score 10; DB 1; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CN 2  
|:  
2 CD 3

## RESULT 10

TMOF\_SARBU ID TMOF\_SARBU STANDARD; PRT; 6 AA.  
AC P41435;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 01-FEB-1996 (Rel. 33, Last annotation update)  
DE Trypsin-modulating oostatic factor (TMOF).  
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Sarcophagidae; Sarcophaga.  
OX NCBI\_TaxID=7385;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Ovary;  
RX MEDLINE=94211930; PubMed=8159807;  
RA Bylenans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,  
de Loef A.;  
RT Sequencing and characterization of trypsin modulating oostatic  
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria  
(Sarcophaga) bullata.";  
RL Regul. Pept. 50:61-72(1994).  
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis  
in the midgut which indirectly reduces the vitellogenin  
concentration in the hemolymph resulting in inhibition of oocyte  
development.  
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular  
epithelium after a blood meal.  
KW Hormone.  
SQ SEQUENCE 6 AA; 695 MW; 61E72451B7642000 CRC64;

Query Match 19.6%; Score 9; DB 1; Length 6;

Best Local Similarity 40.0%; Pred. No. 1.4e+05;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NEESL 6  
|:  
1 NPTNL 5

## RESULT 11

COM2\_CONPU ID COM2\_CONPU STANDARD; PRT; 8 AA.  
AC P58785;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Leu-contryphan-P.  
OS Conus purpurascens (Purple cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=41690;  
RN [1]  
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
RC STRAIN=Clipperton Island; TISSUE=Venom;  
RX MEDLINE=99388839; PubMed=10461743;  
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,  
Olivera B.M.;  
RT "A novel D-leucine-containing Conus peptide: diverse conformational  
dynamics in the contryphan family.";  
RL J. Pept. Res. 54:93-99(1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
CC -1- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.

CC -1- SIMILARITY: Belongs to the contryphan family.

KW Toxin; Hydroxylation; D-amino acid.

FT DISULFID 2 8  
|:  
MOD RES 4 4 D-LEUCINE.  
SQ SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;

Query Match 19.6%; Score 9; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|:  
2 C 2

## RESULT 12

GLUR\_HUMAN ID GLUR\_HUMAN STANDARD; PRT; 8 AA.  
AC P02729;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Urine glycopeptide.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=72062338; PubMed=5126885;

RA Lote C.J., Weiss J.B.;

RT Identification in urine of a low-molecular-weight highly polar

glycopeptide containing cysteinyl-galactose.";

RL Biochem. J. 123:25P-25P(1971).

CC -1- FUNCTION: The identity of the glycoprotein from which this peptide

is derived is unknown. No physiological function has been

attributed. An erythrocyte membrane glycopeptide having a

similar structure has also been found.

CC PIR; A03188; XGHUEU.

DR GO; GO:0005576; C:extracellular; NAS.

KW Glycoprotein.

FT CARBOHYD 1 1 S-LINKED (GAL. . .).

SQ SEQUENCE 8 AA; 855 MW; C2D87AALF5B1EB1E CRC64;

Query Match 19.6%; Score 9; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.4e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 C 1  
|:  
1 C 1

## RESULT 13

ACPH\_RABIT ID ACPH\_RABIT STANDARD; PRT; 6 AA.  
AC P251E4;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAY-1992 (Rel. 22, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AARE) (Acyl-peptide  
hydrolase) (APH) (Acylaminoacyl-peptidase) (Fragment).  
GN APEH.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE.

RX MEDLINE=92222120; PubMed=1807161;

RA Krishna R.G., Chin C.C.Q., Mold F.;

RT "N-terminal sequence analysis of N alpha-acetylated proteins after



RT unlocking with N-acylaminoacyl-peptide hydrolase.";  
RL Anal. Biochem. 199:45-50(1991).  
CC -!- FUNCTION: This enzyme catalyzes the hydrolysis of the N-terminal  
CC peptide bond of an N-acetylated peptide to generate an N-  
CC acetylated amino acid and a peptide with a free N-terminus. It  
CC preferentially cleaves off Ac-Ala, Ac-Met and Ac-Ser.  
CC -!- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid  
CC + peptide.  
CC -!- SUBUNIT: Homotetramer.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to peptidase family S9C.  
DR PIR; A49792; A49792.  
DR MEROPS; S09.004; -.  
DR InterPro; IPR002471; Pept S9 AS.  
DR PROSITE; PS00708; PRO\_ENDOPEP\_SER; PARTIAL.  
KW Hydrolase; Acetylation.  
FT MOD\_RES 1 1 ACETYLIATION.  
FT NON\_TER 6 6  
SQ SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;  
  
Query Match 17.4%; Score 8; DB 1; Length 6;  
Best Local Similarity 20.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
  
QY 3 EESLI 7  
Db |::  
2 ERQVL 6  
  
RESULT 14  
ASP2\_LACSN  
ID ASP2\_LACSN STANDARD; PRT; 6 AA.  
AC P82655;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Acid shock protein 2 (Fragment).  
OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1625;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CBI;  
RX MEDLINE=21322712; PubMed=11429463;  
RA De Angelis M., Bini L., Pallini V., Cocconcelli P.S., Gobbetti M.;  
RT "The acid-stress response in Lactobacillus sanfranciscensis CBI.";  
RL Microbiology 147:1863-1873(2001).  
CC -!- INDUCTION: Overexpressed in acid environments.  
FT NON\_TER 6 6  
SQ SEQUENCE 6 AA; 778 MW; 6AA45B5B132A8000 CRC64;  
  
Query Match 17.4%; Score 8; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 2 NE 3  
Db |:  
5 ND 6  
  
RESULT 15  
CCF1\_ENTFA  
ID CCF1\_ENTFA STANDARD; PRT; 7 AA.  
AC P20104;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last annotation update)  
DE Sex pheromone cCF10.  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]

RP SEQUENCE  
RX MEDLINE=89008313; PubMed=3139658;  
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
RA Adsit J.C., Dunny G.M., Suzuki A.;  
RT "Structure of cCF10, a peptide sex pheromone which induces  
RT conjugative transfer of the Streptococcus faecalis tetracycline  
RT resistance plasmid, pCF10.";  
RL J. Biol. Chem. 263:14574-14578(1988).  
CC -!- FUNCTION: CCF10 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE  
CC PIR; A30812; A30812.  
DR Pheromone.  
KW SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;  
  
Query Match 17.4%; Score 8; DB 1; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.4e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 5 SLI 7  
Db |::  
3 TLV 5  
  
Search completed: September 5, 2004, 10:38:49  
Job time : 16 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:35:32 ; Search time 57 Seconds  
(without alignments)  
44.283 Million cell updates/sec

Title: US-09-761-636A-6  
Perfect score: 46  
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 488

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	39.1	8	10	Q9SAV7	Q9say7 dioscorea t
2	16	34.8	7	12	Q67113	Q67113 influenzavi
3	16	34.8	7	13	Q42564	Q42564 fugu rubrip
4	14	30.4	8	4	Q81V87	Q81v87 homo sapien
5	13	28.3	7	11	Q55184	Q55184 rattus norv
6	13	28.3	8	2	Q32560	Q32560 escherichia
7	12	26.1	8	2	Q3ZEZ9	Q3ze29 buchnera ap
8	12	26.1	8	4	Q9BYR5	Q9byr5 homo sapien
9	12	26.1	8	4	Q15895	Q15895 homo sapien
10	12	26.1	8	4	Q15890	Q15890 homo sapien
11	12	26.1	8	6	Q9BF82	Q9bf82 ursus arcto
12	12	26.1	8	6	Q9BFC2	Q9bfc2 macropus eu
13	12	26.1	8	6	Q9BF90	Q9bf90 tragelaphus
14	12	26.1	8	6	Q9BFB1	Q9bfb1 echinops te
15	12	26.1	8	6	Q9BF93	Q9bf93 megaptera n
16	12	26.1	8	6	Q9BFA1	Q9bfa1 ateles fusc

17	12	26.1	8	6	Q9BF87	Q9bf87 tapirus ind
18	12	26.1	8	6	Q9BF89	Q9bf89 euphractus
19	12	26.1	8	6	Q9BF88	Q9bf88 chaetophrac
20	12	26.1	8	6	Q9BFA0	Q9bfa0 macaca mula
21	12	26.1	8	6	Q9BFA8	Q9bfa8 loxodonta a
22	12	26.1	8	6	Q9BFA9	Q9bfa9 procavia ca
23	12	26.1	8	6	Q9BFB2	Q9bfb2 sorex arane
24	12	26.1	8	6	Q9BFB5	Q9bfb5 erinaceus c
25	12	26.1	8	6	Q9BFB6	Q9bfb6 myrmecophag
26	12	26.1	8	6	Q9BFB3	Q9bfb3 condylura c
27	12	26.1	8	6	Q9BF88	Q9bf88 equus cabal
28	12	26.1	8	6	Q9BF95	Q9bf95 roussetus l
29	12	26.1	8	6	Q9BF99	Q9bf99 hyllobates c
30	12	26.1	8	6	Q9BF84	Q9bf84 panthera on
31	12	26.1	8	6	Q9BFC3	Q9bfc3 didelphis m
32	12	26.1	8	6	Q9BFA4	Q9bfa4 tupia mino
33	12	26.1	8	6	Q9BFA2	Q9bfa2 tarsius ban
34	12	26.1	8	6	Q9BF85	Q9bf85 leopardus p
35	12	26.1	8	6	Q9BFC1	Q9bfc1 choleopus h
36	12	26.1	8	6	Q9BF89	Q9bf89 okapia john
37	12	26.1	8	6	Q9BF96	Q9bf96 pteropus gi
38	12	26.1	8	6	Q9BF80	Q9bf80 trichechus
39	12	26.1	8	6	Q9BF86	Q9bf86 felis silve
40	12	26.1	8	6	Q9BF92	Q9bf92 tursiops tr
41	12	26.1	8	6	Q9BF87	Q9bf87 tamandua te
42	12	26.1	8	6	Q9BF91	Q9bf91 hippopotamu
43	12	26.1	8	6	Q9BF84	Q9bfb4 talpa alta
44	12	26.1	8	6	Q9BFC0	Q9bfc0 choleopus d
45	12	26.1	8	6	Q9BF98	Q9bf98 callimico g

#### ALIGNMENTS

#### RESULT 1

Q9SAY7 PRELIMINARY; PRT; 8 AA.

AC Q9SAY7; DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

DE Phosphoglucose isomerase (Fragment).

OS Dioscorea tokoro.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;

OC Dioscorea.

OX NCBI\_TaxID=64475;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DT17-1;

EX MEDLINE=20279211; PubMed=10821191;

RA Terauchi K., Kahl G.;

RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking

RT regions of Pal and Pgi genes from yams (Dioscorea).";

RL Mol. Gen. Genet. 263:554-560(2000).

DR EMBL; AB016716; BAA32235.1;

DR GO; GO:0016833; F:isomerase activity; IEA.

KW isomerase.

FT NON TER

SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;

Query Match 39.1%; Score 18; DB 10; Length 8;  
Best Local Similarity 75.0%; Pred. No. le+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 SLIC 8  
Db 5 TLIC 8

#### RESULT 2

Q67113 PRELIMINARY; PRT; 7 AA.

ID Q67113

Q67113;  
 AC 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DE 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
 DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end (Fragment).  
 DE (Fragment).  
 OS Influenzavirus A.  
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;  
 OC Influenza A viruses.  
 OX NCBI\_TaxID=197911;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=81001892; PubMed=7407922;  
 RX Dhar R., Chanock R.M., Lai C.-J.,  
 RA "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza RT viral mRNA deduced from cloned complete genomic sequences.";  
 RT Cell 21:495-500(1980).  
 RL EMBL; M25045; AAA43202.1; -.  
 DR NON\_TER 1  
 FT SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;  
 SQ  
 Query Match 34.8%; Score 16; DB 12; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
 QY 1 CNEESLIC 8  
 Db |||||  
 3 CN-----IC 6  
 RESULT 3  
 O42564 PRELIMINARY; PRT; 7 AA.  
 ID O42564;  
 AC O42564;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
 GN SCN8A.  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Takifugu.  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97442476; PubMed=9295353;  
 RX Plummer N.W., McBurney M.W., Meisler M.H.;  
 RA "Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";  
 RT J. Biol. Chem. 272:24008-24015(1997).  
 RL EMBL; U97673; AAB80916.1; -.  
 DR GO; GO:0005216; Filon channel activity; IEA.  
 KW Ionic channel.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;  
 Query Match 34.8%; Score 16; DB 13; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 LIC 8  
 Db |||||  
 3 LVC 5  
 RESULT 4  
 Q81V87 PRELIMINARY; PRT; 8 AA.  
 ID Q81V87;  
 AC Q81V87;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit 2-like (Aminotransferase 2), variant 1) (Fragment).  
 DE SPTLC2L.  
 GN Homo sapiens (Human).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP Smith M.;  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AL050320; CAD54807.1; -.  
 DR GO; GO:0016740; F:transferase activity; IEA.  
 KW Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 8 AA; 908 MW; 8E533682CEBEB042 CRC64;  
 Query Match 30.4%; Score 14; DB 4; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 LIC 8  
 Db |||||  
 1 VIC 3  
 RESULT 5  
 O55184 PRELIMINARY; PRT; 7 AA.  
 ID O55184;  
 AC O55184;  
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Orphan receptor TR4-NS (Fragment).  
 GN TR4.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RX MEDLINE=96198747; PubMed=8612486;  
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
 RA Detera-Wadleigh S.D.;  
 RT "Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal domain.";  
 RL Endocrinology 137:1562-1571(1996).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Sprague-Dawley;  
 RX MEDLINE=96299786; PubMed=8661150;  
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;  
 RT "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene.";  
 RL Genomics 35:361-366(1996).  
 RL EMBL; U59454; AAB91433.1; -.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;  
 Query Match 28.3%; Score 13; DB 11; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 IC 8  
 Db |||||  
 2 IC 3

```

RESULT 6
O32560
ID Q32560 PRELIMINARY; PRT; 8 AA.
AC Q32560;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Propionate kinase (Fragment).
GN TDCD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=W3110;
RX MEDLINE=99449059; PubMed=10520749;
RA Hessleringer C., Sawers G.;
RT "The tdcE gene in Escherichia coli W3110 is separated from the rest of
RT the tdc operon by insertion of IS5 elements.";
RL DNA Seq. 9:183-188(1998).
DR EMBL; AJ001620; CAA04875.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match 28.3%; Score 13; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 IC 8
Db 5 IC 6

RESULT 7
O9ZEZ9 PRELIMINARY; PRT; 8 AA.
ID Q9ZEZ9;
AC Q9ZEZ9;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN LEUA.
OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEMS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006874; CAA07290.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR GO; GO:0003852; F:2-isopropylmalate synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON_TER 8
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 26.1%; Score 12; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 NEESLI 7
Db 2 NSQVII 7

```

```

RESULT 8
Q9BYV5 PRELIMINARY; PRT; 8 AA.
ID Q9BYV5;
AC Q9BYV5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Bizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011664; AAG47575.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0003677; F:DNA binding; NAS.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
FT NON_TER 1
SQ SEQUENCE 8 AA; 1006 MW; DF02C331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db 2 LYC 4

RESULT 9
Q15895 PRELIMINARY; PRT; 8 AA.
ID Q15895;
AC Q15895;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE (Clone XP6A10A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32075; AAA73885.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 921 MW; C6C735B33686C1AA CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 ESLI 7
Db 5 KSLV 8

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RESULT 10
Q15890
ID Q15890 PRELIMINARY; PRT; 8 AA.
AC Q15890;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (Clone XP19G12A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindeay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32083; AAA73880.1; -.
FT NON_TER 1
FT NON_TER 8
FT NON_TER 1
SQ SEQUENCE 8 AA; 975 MW; 605EA6C5BEA5A2D3 CRC64;

Query Match 26.1%; Score 12; DB 4; Length 8;
Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNE 3
Db |::
4 CSQ 6

RESULT 11
Q9BF82
ID Q9BF82 PRELIMINARY; PRT; 8 AA.
AC Q9BF82;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE cAMP responsive element moderator (Fragment).
GN CREM.
OS Ursus arctos (Brown bear) (Grizzly bear).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=9644;
RN [1]_TaxID=9644;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011683; AAG47591.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 12
Q9BFC2
ID Q9BFC2 PRELIMINARY; PRT; 8 AA.
AC Q9BFC2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]_TaxID=9315;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011621; AAG47536.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 13
Q9BF90
ID Q9BF90 PRELIMINARY; PRT; 8 AA.
AC Q9BF90;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Tragelaphus eurycerus (Bongo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Tragelaphus.
OX NCBI_TaxID=69297;
RN [1]_TaxID=69297;
RP SEQUENCE FROM N.A.
RX MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011673; AAG47583.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8
Db |::
2 LYC 4

RESULT 14
Q9BF81
ID Q9BF81 PRELIMINARY; PRT; 8 AA.
AC Q9BF81;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE CAMP responsive element moderator (Fragment).
GN CREM.
OS Echinops telfairi (Lesser hedgehog tenrec).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

OC Mammalia; Eutheria; Insectivora; Tenrecidae; Tenrecinae; Echinops.  
 OX NCBI\_TaxID=9371;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL; AY011632; AAG47547.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 8 AA; 978 MW; DF1DD331EEAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8  
 Db | |  
 2 LYC 4

## RESULT 15

Q9BF93 PRELIMINARY; PRT; 8 AA.  
 AC Q9BF93;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE CAMP responsive element moderator (fragment).  
 GN CREW.  
 OS Megaptera novaeangliae (Humpback whale).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;  
 OC Balaenopteridae; Megaptera.  
 OX NCBI\_TaxID=9773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21082082; PubMed=11214319;  
 RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,  
 RA O'Brien S.J.;  
 RT "Molecular phylogenetics and the origins of placental mammals.";  
 RL Nature 409:614-618(2001).  
 DR EMBL; AY011669; AAG47580.1; -.  
 FT NON TER 1 1  
 SQ SEQUENCE 8 AA; 1025 MW; DF02C3240EAB572A CRC64;

Query Match 26.1%; Score 12; DB 6; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 LIC 8  
 Db | |  
 2 LYC 4

Search completed: September 5, 2004, 10:39:53  
 Job time : 58 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:32:27 ; Search time 63 Seconds  
(without alignments)  
35.879 Million cell updates/sec

Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 122046

Minimum DB seq length: 0

Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	8	AAU04525	AAU04525 VEGF base
2	43	93.5	8	AAU04539	AAU04539 VEGF base
3	42	91.3	8	AAU04541	AAU04541 VEGF base
4	41	89.1	8	AAU04538	AAU04538 VEGF base
5	39	84.8	8	AAU04540	AAU04540 VEGF base
6	30	65.2	8	AAU24954	AAU24954 Conformet
7	30	65.2	8	AAU54526	AAU54526 Human CD4
8	26	56.5	8	AAU73351	AAU73351 Human TSH
9	26	56.5	8	AAU73350	AAU73350 Human TSH
10	26	56.5	8	AAU57040	AAU57040 Peline im
11	26	56.5	8	AAU08451	AAU08451 Peptide A
12	25	54.3	8	AAU80365	AAU80365 Protein p
13	25	54.3	8	AAU49750	AAU49750 Glutamine
14	25	54.3	8	AAU48644	AAU48644 Membrane
15	25	54.3	8	ABG35021	ABG35021 Endostati
16	24	52.2	8	AAU08460	AAU08460 Peptide C
17	23	50.0	7	AAU25915	AAU25915 Beta-2-mi
18	23	50.0	8	AAU73349	AAU73349 Human TSH
19	23	50.0	8	AAU73348	AAU73348 Human TSH
20	23	50.0	8	AAU12848	AAU12848 RGD-bind
21	23	50.0	8	AAU48852	AAU48852 Membrane
22	23	50.0	8	AAU48662	AAU48662 Membrane
23	23	50.0	8	AAU48640	AAU48640 Membrane
24	23	50.0	8	AAU06526	AAU06526 Claudin-2
25	23	50.0	8	AAU17353	AAU17353 Integrin-

## ALIGNMENTS

## RESULT 1

AAU04525  
ID AAU04525 standard; peptide; 8 AA.

XX AC AAU04525;

XX XX 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 2.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;

XX KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX PH Key Location/Qualifiers

XX FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"

XX XX WO200152875-A1.

XX XX 26-JUL-2001.

XX XX 18-JAN-2001; 2001WO-US001533.

XX XX 18-JAN-2000; 2000US-0176293P.

XX XX 16-MAY-2000; 2000US-0204590P.

XX XX (LUDW-) LUDWIG INST CANCER RES.

XX XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX XX WPI; 2001-442248/47.

XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX PS Claim 49; Page 32; 102pp; English.

XX CC The sequence represents a monomeric monocyclic peptide of the invention, whose 3-dimensional structure is modelled on the exposed loop of human VEGFD (vascular endothelial growth factor). The invention relates to a method of producing a monomeric monocyclic peptide by a measuring beta-beta carbon separation distances on opposite antiparallel strands of a

CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation, diabetes induced neovascular  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 8 AA;

Query Match 100.0%; Score 46; DB 4; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 |||||  
 Db 1 CNEESLIC 8

RESULT 2  
 AAU04539  
 ID AAU04539 standard; peptide; 8 AA.

XX AC AAU04539;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 17.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Disulfide-bond 1. .8

FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX XX (LUDW-) LUDWIG INST CANCER RES.

XX XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX XX WPI; 2001-442248/47.

XX DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine

PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 PS  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 8 AA;

Query Match 93.5%; Score 43; DB 4; Length 8;  
 Best Local Similarity 87.5%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 |||||  
 Db 1 CNEETLIC 8

RESULT 3

AAU04541

ID AAU04541 standard; peptide; 8 AA.

XX AC AAU04541;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based monocyclic peptide 19.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers  
 FT Disulfide-bond 1. .8

FT /note= "This bond cyclises the peptide"

XX PN WO200152875-A1.

XX PD 26-JUL-2001.

XX PF 18-JAN-2001; 2001WO-US001533.

XX PR 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX XX

PA (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 PS The sequence represents a monomeric monocyclic peptide of the invention,  
 XX whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX SQ Sequence 8 AA;  
 Query Match 91.3%; Score 42; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNEESLIC 8  
 |||||:  
 Db 1 CNEESVVC 8  
 RESULT 4  
 AAU04538  
 ID AAU04538 standard; peptide; 8 AA.  
 XX AC AAU04538;  
 XX 26-SEP-2001 (first entry)  
 DE VEGF based monocyclic peptide 16.  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 XX diabetic retinopathy; chronic inflammation; cyclic.  
 OS Synthetic.  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1..8  
 FT /note= "This bond cyclises the peptide"  
 XX

PN WO200152875-A1.  
 XX 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293p.  
 PR 16-MAY-2000; 2000US-0204590p.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 PS The sequence represents a monomeric monocyclic peptide of the invention,  
 XX whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX SQ Sequence 8 AA;  
 Query Match 89.1%; Score 41; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CNEESLIC 8  
 |||||:  
 Db 1 CNEESLVC 8  
 RESULT 5  
 AAU04540  
 ID AAU04540 standard; peptide; 8 AA.  
 XX AC AAU04540;  
 XX 26-SEP-2001 (first entry)  
 DE VEGF based monocyclic peptide 18.  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX Synthetic.

XX Key Location/Qualifiers  
 XX Disulfide-bond 1..8  
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 from an exposed loop of a growth factor protein by oxidizing the cysteine  
 residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,  
 whose 3-dimensional structure is modelled on the expose loop of human  
 VEGF (vascular endothelial growth factor). The invention relates to a  
 method of producing a monomeric monocyclic peptide by a measuring beta-  
 beta carbon separation distances on opposite antiparallel strands of a  
 peptide loop fragment from an exposed loop of a growth factor protein and  
 cyclizing the peptide by oxidising the cysteine residues. The monocyclic  
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 peptides) and a cyclic peptide with at least one amino acid deleted prior  
 to cyclisation are used to interfere with angiogenesis,  
 neovascularisation or lymphangiogenesis in a mammal with a condition  
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 The condition is diabetic retinopathy, psoriasis, arthropathy,  
 hemangioma, vascularised malignant or benign tumour, post-recovery  
 cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 trauma, substance-induced neovascularisation of the liver, excessive  
 hormone-related angiogenic dysfunction, diabetes induced neovascular  
 sequelae, hypertension induced neovascular sequelae, or chronic liver  
 infection. The peptides are also used to modulate vascular permeability  
 in a mammal (the mammal has a condition characterised by fluid  
 accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 or brain). The peptides are used to image blood vessels and lymphatic  
 vasculature. The monomeric and bicyclic peptides are used to interfere  
 with at least one biological activity induced by VEGF, VEGF-C or -D and  
 are also used in combination with an anti-inflammatory agent, to treat a  
 chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 diabetic retinopathy

XX Sequence 8 AA;

Query Match 84.8%; Score 39; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 |||||  
 Db 1 CNEESFIC 8

RESULT 6  
 AAR24954  
 ID AAR24954 standard; protein; 8 AA.

XX AAR24954;  
 XX 25-MAR-2003 (revised)  
 DT 04-DEC-1992 (first entry)  
 XX Conformationally constrained HIV inhibitory peptide.  
 XX Human immunodeficiency virus; AIDS; envelope glycoproteins; CD4;  
 KW cell surface protein; infection.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1..8  
 FT Region 1..2  
 FT /note= "conformationally constraining gp."  
 FT Peptide 3..6  
 FT /note= "beta-turn or beta-turn mimic tetrapeptide"  
 FT Region 7..8  
 FT /note= "conformationally constraining gp."  
 XX WO9209625-A1.

XX 11-JUN-1992.

XX 27-NOV-1991; 91WO-US008873.

XX 29-NOV-1990; 90US-00619782.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (UYCO ) UNIV COLUMBIA NEW YORK.

XX Bhatnagar PK, Jarlais RLD, Dixon JS, Hendrickson WA, Kopple KD;  
 PI Kwong P, Peishoff CE, Ryu SE, Truneh A, Sweet RW;

XX WPI; 1992-217018/26.

XX Conformationally constrained peptides used for inhibiting HIV - by  
 mimicking the stereochemical regions of the CD4 receptor protein.

XX Example; Page 24; 37pp; English.

XX The peptide is conformationally constrained by groups attached to each  
 side. The peptide mimics a beta turn and can bind to at least one HIV  
 envelope protein, thus inhibiting infection. It inhibits the interaction  
 between HIV envelope glycoproteins and human cell-surface protein CD4 by  
 mimicking structures of CD4. See also AAR24950-R24959 and AAR25122.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;

Query Match 65.2%; Score 30; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 |||||  
 Db 1 CMOGSFLC 8

RESULT 7  
 AAY54526  
 ID AAY54526 standard; peptide; 8 AA.

XX AAY54526;

XX 25-APR-2000 (first entry)

XX Human CD4 protein target antigenic peptide pl615.

XX Human; CD4 protein; antigenic peptide; CD4-like domain; apoptosis;  
 KW syncytia formation; human immune deficiency virus; HIV binding;



```

XX      SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 CNEESL 6
DB      3 CNESSM 8

RESULT 10
AAY57040
ID      AAY57040 standard; peptide; 8 AA.
XX
AC
XX      AAY57040;
DT      21-FEB-2000 (first entry)
XX
DE      Feline immunodeficiency virus immunogenic fragment.
XX
KW      Feline immunodeficiency virus; FIV; infection; diagnosis; gp130; p55;
KW      immunogenic fragment; antibody; env precursor; gag precursor; cat;
KW      antibody binding composition.
XX
OS      Feline immunodeficiency virus.
XX
PI      EP962774-A1.
XX
PD      08-DEC-1999.
XX
PF      14-MAY-1999; 99EP-00303760.
XX
PR      15-MAY-1998; 98US-0085615P.
PR      03-JUN-1998; 98US-00089878.
XX
PA      (IDEX-) IDEXX LAB INC.
XX
PI      Groat RG, Mermer B, O'connor TP;
XX
DR      WPI; 2000-025671/03.
XX
PT      Diagnosing Feline Immunodeficiency Virus infection.
XX
PS      Disclosure; Page 4; 15pp; English.
XX
CC      This sequence is an immunogenic fragment of feline immunodeficiency virus
CC      (FIV) glycoprotein 130. Peptides AAY57038-Y57039 (also fragments of
CC      gp130) are used in the invention as capture polypeptides when diagnosing
CC      FIV infection. The invention relates to an antibody binding composition
CC      which consists of an enhanced capture polypeptide, which contains an
CC      immunogenic fragment of FIV gag precursor p55, and a second fragment
CC      which is part of the env precursor gp130, and an antibody-binding
CC      detection composition. The invention also includes a device for
CC      performing an assay which determines whether a feline is infected with
CC      FIV. The novel method is used for the diagnosis of Feline
CC      Immunodeficiency Virus infection
XX
SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 3; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.4e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 CNEESLIC 8
DB      1 CNQNPFFC 8

RESULT 11
AAU08451
ID      AAU08451 standard; peptide; 8 AA.

XX      AC      AAU08451;
XX      DT      21-NOV-2001 (first entry)
XX      DE      Peptide A6 encoded by human VEGF-A forward primer A6-F.
XX      KW      Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;
XX      angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
XX      age-related macular degeneration; rheumatoid arthritis; cardiovascular;
XX      primer; mutant; mutein.
XX      OS      Homo sapiens.
XX      SX      Synthetic.
XX      PN      WO200162942-A2.
XX      PD      30-AUG-2001.
XX      PF      26-FEB-2001; 2001WO-US0061113.
XX      PR      25-FEB-2000; 2000US-0185205P.
XX      PR      18-MAY-2000; 2000US-0205331P.
XX      PA      (LUDW-) LUDWIG INST CANCER RES.
XX      PA      (LICN) LICENTIA OY.
XX      PI      Alitalo K, Jeltsch MM;
XX      DR      WPI; 2001-536640/59.
XX      DR      N-PSDB; AAS12807.
XX      PT      Polypeptides that bind cellular receptors for vascular endothelial growth
XX      factors, polynucleotides encoding them.
XX      PS      Claim 9; Fig 7C; 261pp; English.
XX      CC      The present invention relates to polypeptides that bind cellular
XX      receptors for vascular endothelial growth factors (VEGFs), the
XX      polynucleotides encoding them, and their use for identifying agents that
XX      modulate interactions between VEGFs and their receptors. VEGFs and their
XX      receptors play an important role in vasculogenesis, the development of
XX      the embryonic vasculature from early differentiating endothelial cells
XX      and angiogenesis, the process of forming new blood vessels from pre-
XX      existing ones. Modulators of interactions between VEGF and its receptors
XX      may be used to treat dysfunction of the endothelial cell regulatory
XX      system. Such disorders include cancer, abnormal angiogenesis,
XX      proliferative retinopathies, age-related macular degeneration, rheumatoid
XX      arthritis and psoriasis. The polypeptides of the invention exhibit unique
XX      receptor binding profiles compared to known naturally occurring VEGFs.
XX      CC      AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human
XX      VEGF-A forward primers used in the methods of the present invention
XX      SQ      Sequence 8 AA;
Query Match          56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY      1 CNEESL 6
DB      3 CNEDEGL 8

RESULT 12
AAR80365
ID      AAR80365 standard; peptide; 8 AA.
XX
AC      AAR80365;
XX
DT      19-APR-1996 (first entry)
XX
DE      Protein polymeric adhesion substrate glutamine donor peptide #15.

```

XX KW Pendent group; repeating unit; enzyme recognition site; sealant; fibrin;  
 XX KW enzymatic cross-linking; biocompatible material; structural integrity;  
 XX KW medical adhesive; wound closure; tissue repair; transglutaminase;  
 XX KW protein polymer adhesive substrate.  
 XX OS Synthetic.  
 XX PN WO9523611-A1.  
 XX PD 08-SEP-1995.  
 XX PF 03-MAR-1995; 95WO-US002728.  
 XX PR 03-MAR-1994; 94US-00205518.  
 XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.  
 XX PI Cappello J;  
 XX DR WPI; 1995-320413/41.  
 XX PT Protein polymers comprising repeating units and sequences - capable of  
 PT enzyme-catalysed covalent bond formation useful as a biocompatible  
 PT material for wound closure and tissue repair.  
 XX PS Example 9; Page 75; 138pp; English.  
 XX CC The peptides AAR80351-70 are examples of glutamine donor peptides which  
 CC can be used to generate protein polymeric adhesion substrate (PPAS)  
 CC conrg. repeats of non-fibrin cross-linking donor peptide sequences (see  
 CC AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be used  
 CC as substrates in enzymatic cross-linking reactions catalysed by a  
 CC transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be  
 CC used in biological systems where in situ formation of a biocompatible  
 CC material with structural integrity is required e.g. as medical adhesives  
 CC and sealants or for wound closure or tissue repair  
 XX SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 | : : :  
 Db 1 CGQSKVIC 8

RESULT 13  
 AAW49750  
 ID AAW49750 standard; peptide; 8 AA.  
 AC AAW49750;  
 XX 25-MAR-2003 (revised)  
 DT 12-OCT-1998 (first entry)  
 XX Glutamine donor peptide.  
 XX Protein polymer; adhesive sealant; wound healing; cross-linking.  
 XX Synthetic.  
 XX US5773577-A.  
 XX 30-JUN-1998.  
 XX 02-MAR-1995; 95US-00397633.  
 XX 03-MAR-1994; 94US-00205518.  
 XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX Cappello J;  
 XX WPI; 1998-387091/33.  
 XX New recombinant protein polymers - containing naturally occurring  
 PT repetitive units for crosslinking by enzymes, useful as medical adhesives  
 PT and sealants, depots and matrices.  
 XX PS Example 9; Col 49; 70pp; English.  
 XX CC This is an example of a glutamine donor peptide that can be utilised in  
 CC novel recombinant protein polymers of the invention. Such polymers (see  
 CC AAW49710-28) typically comprise a repetitive amino acid backbone of  
 CC repetitive units having a collagen, fibroin, elastin or keratin motif and  
 CC at least 2 enzyme recognition sequences comprising a glutamine and/or  
 CC lysine capable of enzyme catalysed isopeptide formation. The polymers are  
 CC capable of covalent crosslinking by enzymatic reaction to form products  
 CC which set quickly and have good adhesive properties and high strength.  
 CC They can be used as medical adhesives and sealants, in the closure of  
 CC wounds and repair of damaged tissues, prostheses coatings, drug depots,  
 CC and matrices for the transplantation of cells. (Updated on 25-MAR-2003 to  
 CC correct PF field.)  
 XX SQ Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 | : : :  
 Db 1 CGQSKVIC 8

RESULT 14  
 AAY48644  
 ID AAY48644 standard; peptide; 8 AA.  
 AC AAY48644;  
 XX 20-MAR-2003 (revised)  
 DT 10-DEC-1999 (first entry)  
 XX Membrane dipeptidase-binding lung homing peptide #15.  
 XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX WO9946284-A2.  
 XX 16-SEP-1999.  
 XX 10-MAR-1999; 99WO-US005284.  
 XX 13-MAR-1998; 98US-00042107.  
 PR 26-FEB-1999; 99US-00258754.  
 XX (BURN-) BURNHAM INST.  
 XX Rajotte D, Pasqualini R, Ruoslahti EI;  
 WPI; 1999-571717/48.  
 XX New peptides which selectively home to organs or tissues, used for, e.g.  
 PT identifying target ligands and for therapy of pathological conditions.  
 XX Example 6; Page 144; 193pp; English.

CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP) RAY49618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)

XX Sequence 8 AA;

Query Match 54.3%; Score 25; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 | | | |  
 Db 1 CGNETLRC 8

# RESULT 15

ABG35021  
 ID ABG35021 standard; peptide; 8 AA.

XX AC ABG35021;

XX DT 15-JUL-2002 (first entry)

XX DE Endostatin targeting peptide #20.

XX KW Targeting peptide; cancer; Hodgkin's disease; cytostatic;  
 XX immunosuppressive; anti-inflammatory; antiarthritic; antiviral;  
 XX antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;  
 XX inflammatory disease; arthritis; atherosclerosis; cancer;  
 XX autoimmune disease; bacterial infection; viral infection.

XX OS Unidentified.

XX FN WO200220722-A2.

XX PD 14-MAR-2002.

XX PF 07-SEP-2001; 2001WO-US027702.

XX PR 08-SEP-2000; 2000US-0231266P.

XX PR 17-JAN-2001; 2001US-00765101.

XX PA (TEXA ) UNIV TEXAS SYSTEM.

XX PI Arap W, Pasqualini R;

XX DR WPI; 2002-383050/41.

XX Identifying targeting peptides useful for treating e.g. diabetes  
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,  
 PT comprises exposing a sample to a phage display library and recovering  
 PT phage bound to the sample.

XX Claim 56; Page 242; 298pp; English.

XX This invention relates to a novel method for identifying disease  
 CC targeting peptides. The method comprises exposing a sample from an organ,  
 CC tissue or cell type of interest, to a phage display library and  
 CC recovering phage bound to the sample (the phage expresses targeting  
 CC peptides). The peptides identified by the method of the invention may  
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,  
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral  
 CC activities. The methods and composition are useful for identifying  
 CC targeting peptides and one or more receptors for a targeting peptide. The  
 CC targeting peptides are used for selective delivery of therapeutic agents,  
 CC including gene therapy vectors and fusion proteins, to specific organs,  
 CC tissues, or cell types in subject. The targeting peptide may also be used

CC for treating diseases such as diabetes mellitus, inflammatory diseases,  
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and  
 CC viral infections and Hodgkin's disease. The present sequence represents a  
 CC targeting peptide of the invention

XX Sequence 8 AA;

Query Match 54.3%; Score 25; DB 5; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 1.4e+06;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
 | | | |  
 Db 1 CSRSSFLC 8

Search completed: September 5, 2004, 10:38:28  
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(without alignments)  
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Title: US-09-761-636A-6

Perfect score: 46

Sequence: 1 CNEESLIC 8

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3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	8	9 US-09-761-636A-6	Sequence 6, Appli
2	43	93.5	8	9 US-09-761-636A-20	Sequence 20, Appl
3	42	91.3	8	9 US-09-761-636A-22	Sequence 22, Appl
4	41	89.1	8	9 US-09-761-636A-21	Sequence 19, Appl
5	39	84.8	8	9 US-09-761-636A-19	Sequence 21, Appl
6	26	56.5	8	9 US-09-795-006A-133	Sequence 133, App
7	25	54.3	8	12 US-10-363-208-108	Sequence 108, App
8	24	52.2	8	9 US-09-795-006A-142	Sequence 142, App
9	23	50.0	7	10 US-09-827-345-14	Sequence 14, Appl
10	23	50.0	8	9 US-09-840-277-25	Sequence 25, Appl
11	23	50.0	8	9 US-09-185-908-115	Sequence 115, App
12	23	50.0	8	12 US-10-609-217-457	Sequence 457, App
13	23	50.0	8	12 US-10-363-208-74	Sequence 74, Appl
14	23	50.0	8	12 US-10-363-208-82	Sequence 82, Appl
15	23	50.0	8	12 US-10-632-388-457	Sequence 457, App

16	23	50.0	8	12	US-10-651-723-457	Sequence 457, App
17	23	50.0	8	12	US-10-645-761-457	Sequence 457, App
18	23	50.0	8	16	US-10-666-636-457	Sequence 457, App
19	23	50.0	8	16	US-10-653-048-457	Sequence 457, App
20	22	47.8	6	14	US-10-006-869-3664	Sequence 3664, Ap
21	22	47.8	6	15	US-10-395-032-3664	Sequence 3664, Ap
22	22	47.8	7	14	US-10-006-869-3665	Sequence 3665, Ap
23	22	47.8	7	14	US-10-190-082-92	Sequence 92, Appl
24	22	47.8	7	15	US-10-395-032-3665	Sequence 3665, Ap
25	22	47.8	8	14	US-10-006-869-1071	Sequence 1071, Ap
26	22	47.8	8	14	US-10-006-869-3624	Sequence 3624, Ap
27	22	47.8	8	15	US-10-395-032-1071	Sequence 1071, Ap
28	22	47.8	8	15	US-10-395-032-3624	Sequence 3624, Ap
29	21	45.7	5	14	US-10-006-869-3663	Sequence 3663, Ap
30	21	45.7	5	15	US-10-395-032-3663	Sequence 985, App
31	21	45.7	6	14	US-10-006-869-985	Sequence 985, App
32	21	45.7	6	14	US-10-006-869-2242	Sequence 2242, Ap
33	21	45.7	6	15	US-10-395-032-985	Sequence 985, App
34	21	45.7	6	15	US-10-395-032-2242	Sequence 2242, Ap
35	21	45.7	7	14	US-10-006-869-989	Sequence 989, App
36	21	45.7	7	15	US-10-006-869-2246	Sequence 2246, Ap
37	21	45.7	7	15	US-10-395-032-989	Sequence 989, App
38	21	45.7	7	15	US-10-395-032-2246	Sequence 2246, Ap
39	21	45.7	8	9	US-09-185-908-221	Sequence 221, App
40	21	45.7	8	12	US-10-363-208-77	Sequence 77, Appl
41	21	45.7	8	13	US-10-012-756-36	Sequence 36, Appl
42	21	45.7	8	14	US-10-094-401-175	Sequence 175, App
43	21	45.7	8	14	US-10-140-164-9	Sequence 9, Appli
44	21	45.7	8	14	US-10-140-164-39	Sequence 39, Appl
45	21	45.7	8	14	US-10-006-869-2160	Sequence 2160, Ap

## ALIGNMENTS

RESULT 1  
US-09-761-636A-6  
; Sequence 6, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-636A-6

Query Match 100.0%; Score 46; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CNEESLIC 8  
Db 1 CNEESLIC 8

RESULT 2  
US-09-761-636A-20  
; Sequence 20, Application US/09761636A  
; Patent No. US20020065218A1

GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 20  
; TYPE: PRT  
; LENGTH: 8  
; ORGANISM: synthetic construct  
US-09-761-636A-20

Query Match 93.5%; Score 43; DB 9; Length 8;  
Best Local Similarity 87.5%; Pred. No. 1.2e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
DB 1 CNEESLIC 8

RESULT 3  
US-09-761-636A-22  
; Sequence 22, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 22  
; TYPE: PRT  
; LENGTH: 8  
; ORGANISM: synthetic construct  
US-09-761-636A-22

Query Match 91.3%; Score 42; DB 9; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
DB 1 CNEESVVC 8

RESULT 4  
US-09-761-636A-19  
; Sequence 19, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela

GENERAL INFORMATION:  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 19  
; TYPE: PRT  
; LENGTH: 8  
; ORGANISM: synthetic construct  
US-09-761-636A-19

Query Match 89.1%; Score 41; DB 9; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
DB 1 CNEESLIC 8

RESULT 5  
US-09-761-636A-21  
; Sequence 21, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 21  
; TYPE: PRT  
; LENGTH: 8  
; ORGANISM: synthetic construct  
US-09-761-636A-21

Query Match 84.8%; Score 39; DB 9; Length 8;  
Best Local Similarity 75.0%; Pred. No. 1.2e+06;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
DB 1 CNEESLIC 8

RESULT 6  
US-09-795-006A-133  
; Sequence 133, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205

; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 133  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-795-006A-133

Query Match 56.5%; Score 26; DB 9; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEESL 6  
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Db 3 CNDEGL 8

RESULT 7  
US-10-363-208-108  
; Sequence 108, Application US/10363208  
; Publication No. US20040048243A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting  
; FILE REFERENCE: 005774.P005PCT  
; CURRENT APPLICATION NUMBER: US/10/363,208  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
US-10-363-208-108

Query Match 54.3%; Score 25; DB 12; Length 8;  
Best Local Similarity 37.5%; Pred. No. 1.2e+06;  
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
|:|:|  
Db 1 CSRSFLC 8

RESULT 8  
US-09-795-006A-142  
; Sequence 142, Application US/09795006A  
; Patent No. US20020151680A1  
; GENERAL INFORMATION:  
; APPLICANT: Alitalo et al  
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR  
; FILE REFERENCE: 28967/35977B  
; CURRENT APPLICATION NUMBER: US/09/795,006A  
; CURRENT FILING DATE: 2001-02-26  
; PRIOR APPLICATION NUMBER: US 60/205,331  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: US 60/185,205  
; PRIOR FILING DATE: 2000-02-25  
; NUMBER OF SEQ ID NOS: 175  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 142  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-795-006A-142

Query Match 52.2%; Score 24; DB 9; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESL 6  
|:|:|  
Db 3 CNSEGL 8

RESULT 9  
US-09-827-345-14  
; Sequence 14, Application US/09827345  
; Publication No. US20030021800A1  
; GENERAL INFORMATION:  
; APPLICANT: CHERMANN, JEAN-CLAUDE  
; APPLICANT: LE CONTEL, CAROLE  
; APPLICANT: GALEA, PASCALE  
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING AN  
; TITLE OF INVENTION: INTRACELLULAR PHASE COMPOSITION FOR THE TREATMENT AND  
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF  
; TITLE OF INVENTION: DIAGNOSIS  
; FILE REFERENCE: 065691-0216  
; CURRENT APPLICATION NUMBER: US/09/827,345  
; CURRENT FILING DATE: 2001-04-09  
; PRIOR APPLICATION NUMBER: 09/599,549  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: PCT/FR96/01006  
; PRIOR FILING DATE: 1996-06-28  
; PRIOR APPLICATION NUMBER: 08/973,551  
; PRIOR FILING DATE: 1998-02-19  
; PRIOR APPLICATION NUMBER: FR 95/07914  
; PRIOR FILING DATE: 1995-06-30  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-827-345-14

Query Match 50.0%; Score 23; DB 10; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CNEES 5  
|:|:|  
Db 2 CNPES 6

RESULT 10  
US-09-840-277-25  
; Sequence 25, Application US/09840277  
; Patent No. US20020168363A1  
; GENERAL INFORMATION:  
; APPLICANT: FEIGE, ULRICH  
; APPLICANT: KOHNO, TADAHIKO  
; APPLICANT: LACEY, DAVID LEE  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: INTEGRIN/ADHESION ANTAGONISTS  
; FILE REFERENCE: A-688A  
; CURRENT APPLICATION NUMBER: US/09/840,277  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: 60/198,919  
; PRIOR FILING DATE: 2000-04-21  
; PRIOR APPLICATION NUMBER: 60/201,394

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; PRIOR FILING DATE: 2000-05-03
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Integrin antagonist peptide
US-09-840-277-25

Query Match          50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDGGLMC 8

RESULT 11
US-09-185-908-115
; Sequence 115, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 115
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-115

Query Match          50.0%; Score 23; DB 9; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CRTSSYVC 8

RESULT 12
US-10-609-217-457
; Sequence 457, Application US/10609217
; Publication No. US20040044188A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/609,217
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-609-217-457

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDGGLMC 8

RESULT 13
US-10-363-208-74
; Sequence 74, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-74

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CRASAMVC 8

RESULT 14
US-10-363-208-82
; Sequence 82, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-82

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE
US-10-609-217-457

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 37.5%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CWDGGLMC 8

RESULT 13
US-10-363-208-74
; Sequence 74, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-74

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
DB      1 CRASAMVC 8

RESULT 14
US-10-363-208-82
; Sequence 82, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(8)
; OTHER INFORMATION: synthetic construct
US-10-363-208-82

Query Match          50.0%; Score 23; DB 12; Length 8;
Best Local Similarity 25.0%; Pred. No. 1.2e+06;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 1 CNEESLIC 8  
| : : : |  
Db 1 CRASAMVC 8

## RESULT 15

US-10-632-388-457  
; Sequence 457, Application US/10632388  
; Publication No. US20040053845A1  
; GENERAL INFORMATION:  
; APPLICANT: FRIGE, ULRICH  
; APPLICANT: LIU, CHUAN-FA  
; APPLICANT: CHEETHAM, JANET C.  
; APPLICANT: BOONE, THOMAS CHARLES  
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
; FILE REFERENCE: A-527  
; CURRENT APPLICATION NUMBER: US/10/632,388  
; CURRENT FILING DATE: 2003-07-31  
; PRIOR APPLICATION NUMBER: US/09/428,082B  
; PRIOR FILING DATE: 1999-10-22  
; PRIOR APPLICATION NUMBER: 60/105,371  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 1133  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 457  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: INTEGRIN-BINDING PEPTIDE  
US-10-632-388-457

Query Match 50.0%; Score 23; DB 12; Length 8;  
Best Local Similarity 37.5%; Pred No. 1.2e+06;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : : : |  
Db 1 CWDGGLMC 8

Search completed: September 5, 2004, 10:44:41  
Job time : 67 secs

**This Page Blank (uspto)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:37:23 ; Search time 20 Seconds  
(without alignments)  
20.650 Million cell updates/sec

Title: US-09-761-636A-6  
Perfect score: 46  
Sequence: 1 CNEESLIC 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 71086

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	65.2	8	US-09-100-409A-27	Sequence 27, Appl
2	26	56.5	8	US-09-089-878-3	Sequence 3, Appl
3	25	54.3	8	US-08-397-633A-100	Sequence 100, Appl
4	25	54.3	8	US-09-258-754-49	Sequence 49, Appl
5	25	54.3	8	US-09-042-107-49	Sequence 49, Appl
6	25	54.3	8	US-09-722-250D-49	Sequence 49, Appl
7	23	50.0	7	US-08-973-551-14	Sequence 14, Appl
8	23	50.0	8	US-08-520-535-3	Sequence 3, Appl
9	23	50.0	8	US-09-079-432-3	Sequence 3, Appl
10	23	50.0	8	US-09-258-754-33	Sequence 33, Appl
11	23	50.0	8	US-09-258-754-42	Sequence 42, Appl
12	23	50.0	8	US-09-258-754-214	Sequence 214, Appl
13	23	50.0	8	US-09-042-107-33	Sequence 33, Appl
14	23	50.0	8	US-09-042-107-42	Sequence 42, Appl
15	23	50.0	8	US-09-042-107-214	Sequence 214, Appl
16	23	50.0	8	US-08-160-604-79	Sequence 79, Appl
17	23	50.0	8	US-08-160-604-80	Sequence 80, Appl
18	23	50.0	8	US-09-722-250D-33	Sequence 33, Appl
19	23	50.0	8	US-09-722-250D-42	Sequence 42, Appl
20	23	50.0	8	US-09-722-250D-214	Sequence 214, Appl
21	23	50.0	8	US-09-428-082B-457	Sequence 457, Appl
22	22	47.8	6	US-09-187-859-3664	Sequence 3664, Ap
23	22	47.8	6	US-09-839-542B-3664	Sequence 3664, Ap
24	22	47.8	7	US-09-187-859-3665	Sequence 3665, Ap
25	22	47.8	7	US-09-839-542B-3665	Sequence 3665, Ap
26	22	47.8	8	US-09-258-754-36	Sequence 36, Appl
27	22	47.8	8	US-09-258-754-48	Sequence 48, Appl

Sequence 256, App  
Sequence 36, Appl  
Sequence 48, Appl  
Sequence 256, App  
Sequence 1071, Ap  
Sequence 3624, Ap  
Sequence 1071, Ap  
Sequence 3624, Ap  
Sequence 36, Appl  
Sequence 48, Appl  
Sequence 256, App  
Sequence 11, Appl  
Sequence 3663, Ap  
Sequence 3663, Ap  
Sequence 985, App  
Sequence 2242, Ap  
Sequence 985, App  
Sequence 2242, Ap

## ALIGNMENTS

RESULT 1  
US-09-100-409A-27  
; Sequence 27, Application US/09100409A  
; Patent No. 6090388  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND  
; TITLE OF INVENTION: IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,409A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 1151-4154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-100-409A-27

Query Match 65.2% ; Score 30; DB 3; Length 8;  
Best Local Similarity 50.0% ; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CNEESLIC 8

Db 1 CNOGSFLC 8

```
RESULT 2
US-09-089-878-3
; Sequence 3, Application US/09089878
; Patent No. 6458528
; GENERAL INFORMATION:
; APPLICANT: Groat, Randall G.
; APPLICANT: O'Connor, Thomas P.
; APPLICANT: Mermer, Brian
; TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION
; TITLE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS
; FILE REFERENCE: 00088/111001
; CURRENT APPLICATION NUMBER: US/09/089,878
; CURRENT FILING DATE: 1998-06-03
; EARLIER APPLICATION NUMBER: US 60/085,615
; EARLIER FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Feline immunodeficiency virus
US-09-089-878-3

Query Match          56.5%; Score 26; DB 4; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 1; Mismatches 4; Indels 4; Gaps 0;

QY      1 CNEESLIC 8
Db      1 CQCNQFFC 8

RESULT 3
US-08-397-633A-100
; Sequence 100, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,633A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 100:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-397-633A-100
Query Match          54.3%; Score 25; DB 1; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
Db      1 CQOSKVIC 8

RESULT 4
US-09-258-754-49
; Sequence 49, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-49

Query Match          54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
Db      1 CGNETLRC 8

RESULT 5
US-09-042-107-49
; Sequence 49, Application US/09042107
; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-49

Query Match          54.3%; Score 25; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 CNEESLIC 8
Db      1 CGNETLRC 8
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```

Db      1  CGNETLRC 8

RESULT 6
US-09-722-250D-49
; Sequence 49, Application US/09722250D
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Issues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 49
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-49

Query Match      54.3%; Score 25; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      1  CNEESLIC 8
Db      1  CGNETLRC 8

RESULT 7
US-08-973-551-14
; Sequence 14, Application US/08973551
; Patent No. 6113902
; GENERAL INFORMATION:
; APPLICANT: Chermann, Jean-Claude
; APPLICANT: Le Contel, Carole
; APPLICANT: Galea, Pascale
; TITLE OF INVENTION: VACCINE AGAINST INFECTIOUS AGENTS HAVING
; TITLE OF INVENTION: AN INTRACELLULAR PHASE COMPOSITION FOR THE TREATMENT AND
; TITLE OF INVENTION: PREVENTION OF HIV INFECTIONS, ANTIBODIES AND METHOD OF
; TITLE OF INVENTION: DIAGNOSIS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,551
; FILING DATE: 30-DEC-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: PCT/FR96/01006
; FILING DATE: 28-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9507914
; FILING DATE: 30-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.

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; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 65691/130
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-973-551-14

Query Match      50.0%; Score 23; DB 3; Length 7;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  CNEES 5
Db      2  CNPES 6

RESULT 8
US-08-520-535-3
; Sequence 3, Application US/08520535
; Patent No. 5817750
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,535
; FILING DATE: 28-AUG-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 1794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-520-535-3

Query Match      50.0%; Score 23; DB 2; Length 8;
Best Local Similarity 37.5%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CNEESLIC 8
Db      1  CWDGLMC 8

RESULT 9

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US-09-079-432-3  
; Sequence 3, Application US/09079432  
; Patent No. 5955572  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Structural Mimics of RGD-Binding Sites  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,432  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/520,535  
; FILING DATE: 28-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LA 1794  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: circular  
US-09-079-432-3

Query Match 50.0%; Score 23; DB 2; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : | : |  
Db 1 CWDGGLMC 8

RESULT 10  
US-09-258-754-33  
; Sequence 33, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Diptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-258-754-33

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : | : |  
Db 1 CRHSSSC 8

RESULT 11  
US-09-258-754-42  
; Sequence 42, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Diptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-42

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : | : |  
Db 1 CHEGLTC 8

RESULT 12  
US-09-258-754-214  
; Sequence 214, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Diptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 214  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-214

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 37.5%; Pred. No. 3e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : : : |  
Db 1 CFXSTLLC 8

## RESULT 13

US-09-042-107-33  
; Sequence 33, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-33

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred.No. 3e+05;  
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : : : |  
Db 1 CRHESSC 8

## RESULT 14

US-09-042-107-42  
; Sequence 42, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 42  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-42

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred.No. 3e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : : : |  
Db 1 CHEGYLC 8

## RESULT 15

US-09-042-107-214  
; Sequence 214, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:

; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 214  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-214

Query Match 50.0%; Score 23; DB 3; Length 8;  
Best Local Similarity 37.5%; Pred.No. 3e+05;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CNEESLIC 8  
| : : : |  
Db 1 CFXSTLLC 8

Search completed: September 5, 2004, 10:40:46  
Job time : 20 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:44:49 ; Search time 22 Seconds  
(without alignments)  
48.096 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1327

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	36.1	11	2 D57789	gallbladder stone
2	20	32.8	6	2 I65546	MHC H2-L antigen - mouse (fragment)
3	19	31.1	5	2 A60521	glycogen phosphory
4	18	29.5	10	2 C39191	hypothetical prote
5	17	27.9	8	2 G33098	205K exoantigen -
6	17	27.9	10	2 C39111	IG heavy chain C r
7	17	27.9	10	2 PH0944	T-cell receptor be
8	17	27.9	11	2 S21727	gamma-interferon-1
9	17	27.9	11	2 PH0929	T-cell receptor be
10	16	26.2	4	2 I51049	metallothionein-A
11	16	26.2	9	2 A60356	IG heavy chain CRD
12	16	26.2	9	2 PT0247	118K stomach cance
13	16	26.2	10	2 S62880	polygalacturonase
14	16	26.2	10	2 A61622	vitellogenin, 190k
15	16	26.2	10	2 PH0926	T-cell receptor be
16	16	26.2	10	2 A32195	Tachykinin II - mi
17	16	26.2	11	2 ECLQ2M	paraspinal crystal
18	16	26.2	11	2 S00616	peptide-N4-(N-acet
19	15	24.6	10	2 B59272	IG H chain V-D-J r
20	15	24.6	11	2 PH1584	stathmin - mouse (
21	15	24.6	11	2 PH0042	T-cell receptor be
22	15	24.6	11	2 PH0941	major protein anti
23	14	23.0	5	2 E60274	hypothetical colla
24	14	23.0	6	4 A35039	large granule L3 c
25	14	23.0	7	2 PC1316	hypertrehalosemic
26	14	23.0	8	2 S08996	adipokinetic hormo
27	14	23.0	8	2 B49823	neuropeptide Led-C
28	14	23.0	8	2 B44960	adipokinetic hormo
29	14	23.0	8	2 A33995	

30 14 23.0 8 2 PL0184 capsid protein VP-  
31 14 23.0 8 2 A42057 fibroblast growth  
32 14 23.0 8 2 A35180 neutral proteinase  
33 14 23.0 9 2 B41983 orf downstream to b  
34 14 23.0 9 2 A29477 diuretic neuropept  
35 14 23.0 9 2 I52974 seminal vesicle pr  
36 14 23.0 10 1 XAVI6B angiotensin-conver  
37 14 23.0 10 2 JCI416 hypertrehalosemic  
38 14 23.0 10 2 S09138 hypertrehalosemic  
39 14 23.0 10 2 B33995 hypertrehalosemic h  
40 14 23.0 10 2 PC2171 triacylglycerol li  
41 14 23.0 10 2 PA0050 protein QA10052 -  
42 14 23.0 10 2 B61218 alpha-gliadin 6Ha  
43 14 23.0 10 2 E86128 hypothetical prote  
44 14 23.0 11 1 XASNBA bradykinin-potent  
45 14 23.0 11 2 S58244 pyrroloquinoline q

## ALIGNMENTS

### RESULT 1

D57789  
gallbladder stone matrix protein, 14.5K - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Feb-1996 #sequence\_revision 23-Feb-1996 #text\_change 23-Feb-1996  
C:Accession: D57789

R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, February 1996  
A:Description: The proteins of gallbladder stones.  
A:Reference number: A57789

A:Accession: D57789

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <BIN>

Query Match

Best Local Similarity 36.1%; Score 22; DB 2; Length 11;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10

DB 1 PATSAP 6

### RESULT 2

I65546  
MHC H2-L antigen - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I65546

R:Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.  
Cell 44, 261-272, 1986

A>Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and their

A:Reference number: 152778; MUID:86106202; PMID:3510743

A:Accession: I65546

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6 <RES>

A:Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match

Best Local Similarity 32.8%; Score 20; DB 2; Length 6;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 VPC 11

DB 2 VPC 4

### RESULT 3

A60521

glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)

N:Alternate names: glycogen phosphorylase b  
 C:Species: *Liiza ramada*  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2003  
 C:Accession: A60521  
 R:Bonamusa, L.; Baanante, I.V.  
 Comp. Biochem. Physiol. B 95, 295-301, 1990  
 A:Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle  
 A:Reference number: A60521; PMID:90227907; PMID:2109669  
 A:Accession: A60521  
 A:Molecule type: protein  
 A:Residues: 1-5 <BON>  
 C:Superfamily: glucan phosphorylase  
 C:Keywords: glycogen phosphorylase; hexosyltransferase; phosphoprotein  
 F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 31.1%; Score 19; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ISVPL 5  
 ||||  
 Db 2 ISVPL 5

## RESULT 4

C39191  
 Hypothetical protein 1 (Tetx 5' region) - *Bacteroides fragilis*  
 C:Species: *Bacteroides fragilis*  
 C:Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 30-Sep-1993  
 C:Accession: C39191  
 R:Speer, B.S.; Bedzyk, L.; Salyers, A.A.  
 J. Bacteriol. 173, 176-183, 1991  
 A:Title: Evidence that a novel tetracycline resistance gene found on two *Bacteroides* strains  
 A:Reference number: A39191; PMID:91100280; PMID:1846135  
 A:Accession: C39191  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-10 <SPE>  
 A:Cross-references: GB:M37699

Query Match 29.5%; Score 18; DB 2; Length 10;  
 Best Local Similarity 57.1%; Pred. No. 3.8e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSV 9  
 ||||  
 Db 4 SRPWTST 10

## RESULT 5

G33098  
 20SK exoantigen - malaria parasite (*Plasmodium falciparum*) (fragments)  
 C:Species: *Plasmodium falciparum*  
 C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000  
 C:Accession: G33098  
 R:Nichols, J.H.; Hager, L.P.  
 Submitted to the Protein Sequence Database, May 1990  
 A:Reference number: A33098  
 A:Accession: G33098  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-8 <NIC>

Query Match 27.9%; Score 17; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9  
 ||||  
 Db 2 VPLXLV 7

## RESULT 6

## C39111

Ig heavy chain C region - Pacific hagfish (fragment)  
 C:Species: *Eptatretus stouti* (Pacific hagfish)  
 C:Date: 18-Oct-1991 #sequence\_revision 18-Oct-1991 #text\_change 16-Aug-1996  
 C:Accession: C39111  
 R:Varner, J.; Neame, P.; Litman, G.W.  
 Proc. Natl. Acad. Sci. U.S.A. 88, 1746-1750, 1991  
 A:Title: A serum heterodimer from hagfish (*Eptatretus stoutii*) exhibits structural similarity  
 A:Reference number: A39111; PMID:91156684; PMID:2000382  
 A:Accession: C39111  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-10 <VAR>  
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 5.6e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ISVPL 6  
 ||||  
 Db 4 ISSPL 8

## RESULT 7

PH0944  
 T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)  
 C:Species: *Rattus norvegicus* (Norway rat)  
 C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C:Accession: PH0944  
 R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A:Reference number: PH0891; PMID:92078857; PMID:1836012  
 A:Accession: PH0944  
 A:Molecule type: mRNA  
 A:Residues: 1-10 <GOL>  
 A:Experimental source: complete Freund's adjuvant-immunized lymph node  
 A>Note: the authors translated the codon GAC for residue 9 as Glu  
 C:Keywords: T-cell receptor

Query Match 27.9%; Score 17; DB 2; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 5.6e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CJSVP 5  
 ||||  
 Db 1 CASSP 5

## RESULT 8

S21727  
 gamma-interferon-induced protein IP-30 precursor - human (fragment)  
 C:Species: *Homo sapiens* (man)  
 C:Date: 22-Nov-1993 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
 C:Accession: S21727  
 R:Wei, M.L.; Cresswell, P.  
 Nature 356, 443-446, 1992  
 A:Title: HLA-A2 molecules in an antigen-processing mutant cell contain signal sequence  
 A:Reference number: S21727; PMID:92212461; PMID:1557127  
 A:Accession: S21727  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-11 <WEI>

Query Match 27.9%; Score 17; DB 2; Length 11;  
 Best Local Similarity 37.5%; Pred. No. 6.2e+03;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 ISVPLTSV 9  
 :|||:  
 Db 3 LDVPTAAV 10

```
RESULT 9
PH0929
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0929
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0929
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
C:Keywords: T-cell receptor

Query Match      27.9%; Score 17; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 C1SVPLT 7
| | | | |
Db 1 CASRPGT 7
| | | | |

RESULT 10
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) me
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:91019799; PIDN:CA56466.1; PID:94379328

Query Match      26.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
| |
Db 3 PC 4
| |

RESULT 11
A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60356
R:Shiraishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: protein
A:Residues: 1-9 <SHI>
C:Keywords: glycoprotein

Query Match      26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPLTSV 9
| | | |
Db 1 IPLKPV 6
| | | |
```

```
RESULT 12
PT0247
IG heavy chain CRD3 region (clone 2-106A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0247
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0247
A:Molecule type: DNA
A:Residues: 1-9 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match      26.2%; Score 16; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTS 8
| | |
Db 2 SAPIDS 7
| | |

RESULT 13
S62880
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C:Species: Aspergillus sp.
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S62880
R:Stratillova, E.; Dzurkova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A:Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A:Reference number: S62880; MUID:96196586; PMID:8612742
A:Accession: S62880
A:Molecule type: protein
A:Residues: 1-10 <STR>
C:Keywords: glycosidase; hydrolase
F:4/Active site: Tyr #status predicted

Query Match      26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11
| |
Db 9 PC 10
| |

RESULT 14
A61622
vitellogenin, 190k chain - gypsy moth (fragment)
N:Contains: vitellin
C:Species: Lymantria dispar (gypsy moth)
C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 15-Oct-1999
C:Accession: A61622
R:Hiremath, S.; Eshita, S.
Insect Biochem. Mol. Biol. 22, 605-611, 1992
A:Title: Purification and characterization of vitellogenin from the gypsy moth, Lymantria
A:Reference number: A61622
A:Accession: A61622
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <HIR>
C:Keywords: egg yolk; hemolymph

Query Match      26.2%; Score 16; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 5 PLT 7  
| |  
Db 2 PLT 4

RESULT 15  
PH0926  
T-cell receptor beta chain V-D-J region (isolate 12) - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C:Accession: PH0926  
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A:Reference number: PH0891; MUID:92078857; PMID:1836012  
A:Accession: PH0926  
A:Molecule type: mRNA  
A:Residues: 1-10 <GOL>  
A:Experimental source: concanavalin A-activated lymphoblast  
A>Note: the authors translated the codon AGA for residue 4 as Thr  
C:Keywords: T-cell receptor

Query Match 26.2%; Score 16; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. NO. 8.4e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVP 5  
| |  
Db 1 CASRP 5

Search completed: September 5, 2004, 10:48:24  
Job time : 23 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:40:49 ; Search time 15 seconds  
(without alignments)  
38.185 Million cell updates/sec

Title: US-09-761-636A-7  
Perfect score: 61  
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 441

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	23	37.7	11	1	TIN4_HOPTI	P82654 hoplobatrach
2	19	31.1	11	1	TIN1_HOPTI	P82651 hoplobatrach
3	18	29.5	8	1	COM2_CONPU	P59785 conus purpu
4	17.5	28.7	9	1	MGMT_BOVIN	P29177 bos taurus
5	17	27.9	10	1	UPA4_HUMAN	P30090 homo sapien
6	16	26.2	11	1	CXIL_CONMR	P58807 conus marmo
7	15	24.6	10	1	LPK2_LOCOMI	P1488 locusta mig
8	14	23.0	8	1	AKH_TABAT	P14595 tabanus atr
9	14	23.0	8	1	HTF2_PERAM	P04549 periplaneta
10	14	23.0	8	1	UPA4_HUMAN	P30096 homo sapien
11	14	23.0	9	1	DNF1_LOCOMI	P16339 locusta mig
12	14	23.0	9	1	YBFR_AZOVI	P25825 azotobacter
13	14	23.0	10	1	BPP2_BOTUA	P01022 bothrops ja
14	14	23.0	10	1	HTF2_CARMO	P11385 carausius m
15	14	23.0	10	1	HTF_TABAT	P14596 tabanus atr
16	14	23.0	11	1	BPP3_BOTIN	P30423 bothrops in
17	14	23.0	11	1	BPP4_BOTIN	P30424 bothrops in
18	14	23.0	11	1	BPPB_AGSHA	P01021 agkistrodon
19	14	23.0	11	1	PQOC_PSEFL	P55173 pseudomonas
20	13	21.3	6	1	E101_LITRU	P82096 litoria rub
21	13	21.3	8	1	UPA1_HUMAN	P30087 homo sapien
22	13	21.3	9	1	CONO_CONST	P05487 conus stria
23	13	21.3	10	1	BPP2_BOTIN	P30422 bothrops in
24	13	21.3	10	1	BPP_VIPAS	P31351 vipera aspi
25	13	21.3	10	1	COXH_ONCMY	P80331 oncorhynch
26	13	21.3	10	1	COXQ_SHEEP	P80337 ovis aries
27	13	21.3	10	1	ESTA_SCHGA	P81012 schizaphis
28	13	21.3	10	1	NS1_MVCTU	P81135 mycobacteri
29	12	19.7	7	1	TPFY_PACDA	P83455 pachymedusa
30	12	19.7	8	1	ALL6_CYPDO	P82157 cydia pomon
31	12	19.7	8	1	FUSS_FUSSO	P81010 fusarium so
32	12	19.7	8	1	VGLG_HSV2B	P81780 herpes simp
33	12	19.7	9	1	FAR5_PENNO	P83320 penaeus mon

34 12 19.7 9 1 FLA2\_TREHY P80159 treponema h  
35 12 19.7 9 1 OXYT\_BUFRE P42995 bufo regula  
36 12 19.7 9 1 SAP\_STOVA P24047 stomopneute  
37 12 19.7 10 1 TKL2\_LOCOMI P16224 locusta mig  
38 12 19.7 10 1 UPA8\_HUMAN P30094 homo sapien  
39 12 19.7 11 1 T2P1\_PROVU P31031 proteus vul  
40 11 18.0 6 1 VP19\_HSVIK P23210 herpes simp  
41 11 18.0 7 1 CARP\_MYTED P10420 mytilus edu  
42 11 18.0 7 1 MNP1\_LEPDE P42984 leptinotars  
43 11 18.0 8 1 PPK3\_PERAM P82618 periplaneta  
44 11 18.0 9 1 COXE\_THUOB P80975 thunnus obe  
45 11 18.0 9 1 FAR9\_ASCSU P43172 ascaris suu

## ALIGNMENTS

RESULT 1  
TIN4\_HOPTI  
ID TIN4\_HOPTI STANDARD; PRT; 11 AA.  
AC P82654;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Tigerin-4.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;  
RX PubMed=11031261;  
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,  
RA Devi A.S., Nagakaj R., Sitaram N.;  
RT "Tigerinins: novel antimicrobial peptides from the Indian frog Rana  
RT tigerina".  
RL J. Biol. Chem. 276:2701-2707(2001).  
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,  
CC S.aureus, M.luteus, P.putida and S.cerevisiae.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Skin.  
CC -!- MASS SPECTROMETRY: MW=1247; METHOD=WALDI.  
KW Amphibian defense peptide; Antibiotic.  
FT DISULFID 3 11  
SQ SEQUENCE 11 AA; 1248 MW; 117D8EFD37605DCB CRC64;  
Query Match 37.7%; Score 23; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CISVPL 6  
Db 3 CYAIPL 8  
RESULT 2  
TIN1\_HOPTI  
ID TIN1\_HOPTI STANDARD; PRT; 11 AA.  
AC P82651;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Tigerin-1.  
OS Hoplobatrachus tigerinus (Indian bull frog) (Rana tigerina).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae;  
OC Hoplobatrachus.  
OX NCBI\_TaxID=103373;  
RN [1]  
RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND DISULFIDE BONDS.  
RC TISSUE=Skin secretion;

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RX PubMed-11031261;
RA Purna Sai K., Jagannadham M.V., Vairamani M., Raju N.P.,
RA Devi A.S., Nagaraj R., Sitarum N.;
RT "Tigerlins: novel antimicrobial peptides from the Indian frog Rana
RT tigerina.";
RL J. Biol. Chem. 276:2701-2707(2001).
CC -!- FUNCTION: Antibacterial activity against B.subtilis, E.coli,
CC S.aureus, M.luteus, P.putida and S.cerevisiae.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- MASS SPECTROMETRY: MW=1342; METHOD=MALDI.
KW Amphibian defense peptide; Antibiotic; Fungicide; Amidation.
FT DISULFID 2 10
FT MOD_RES 11 11
FT SEQUENCE 11 AA; 1344 MW; A2087DC960476056 CRC64;
SQ
Query Match 31.1%; Score 19; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.7e+02;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 CISVPL 6
Db | : |
2 CTMIPI 7
RESULT 3
COM2_CONPU STANDARD; PRT; 8 AA.
AC P58785;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Leu-contryphan-P.
OS Conus purpurascens (Purple cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=41690;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC STRAIN=Clipperton Island; TISSUE=Venom;
RX MEDLINE=99388839; PubMed=10461743;
RA Jacobsen R.B., Jimenez E.C., De la Cruz R.G.C., Gray W.R., Cruz L.J.,
RA Olivera B.M.;
RT "A novel D-leucine-containing Conus peptide: diverse conformational
RT dynamics in the contryphan family.";
RL J. Pept. Res. 54:93-99(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- MASS SPECTROMETRY: MW=888.4; METHOD=LSIMS.
CC -!- SIMILARITY: Belongs to the contryphan family.
KW Toxin; Hydroxylation; D-amino acid.
FT DISULFID 2 8
FT MOD_RES 4 4
FT SEQUENCE 8 AA; 890 MW; 75A367672732CEB8 CRC64;
SQ
Query Match 29.5%; Score 18; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CISVP 5
Db | : |
2 CVLLP 6
RESULT 4
MGMT_BOVIN STANDARD; PRT; 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
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DE methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Kazran P.;
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA
RT methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically
CC transferring the alkyl group at the O-6 position to a cysteine
CC residue in the enzyme. This is a suicide reaction: the enzyme is
CC irreversibly inactivated.
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein
CC [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein
CC S-methyl-L-cysteine.
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE
CC WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro; IPR001497; Methyltransf_1.
DR PROSITE; PS00374; MGMT; PARTIAL.
KW DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9
FT NON_TER 9 9
FT SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;
SQ
Query Match 28.7%; Score 17.5; DB 1; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.4e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
QY 4 VPLTSVPC 11
Db | : |
3 IPILT-PC 9
RESULT 5
UPAA_HUMAN STANDARD; PRT; 10 AA.
AC P30090;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 12) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.8, its MW is: 40.5 kDa.
CC -!- MISCELLANEOUS: This spot is on a position thought to be that of
CC Zn-alpha-2 glycoprotein, but it does not correspond to that
CC protein.
DR SWISS-2DPAGE; P30090; HUMAN.
FT NON_TER 1 1
FT UNSURE 4 4
FT NON_TER 10 10
FT SEQUENCE 10 AA; 1067 MW; 269492EB05A1A457 CRC64;
SQ
```

Query Match 27.9%; Score 17; DB 1; Length 10;  
 Best Local Similarity 80.0%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTS 8  
 DB 2 VPNTS 6

RESULT 6  
 ID CKL1 CONMR STANDARD; PRT; 11 AA.  
 AC P58807;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lambda-conotoxin CmrVIA.  
 OS Conus marmoreus (Marble cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=42752;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20564325; PubMed=10988292;  
 RA Balaji K.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
 RA Seow K.T., Bay B.-H.;  
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
 RT pattern and protein folding. Isolation and characterization from the  
 RT venom of Conus marmoreus".  
 RL J. Biol. Chem. 275:39516-39522 (2000).  
 CC -!- FUNCTION: Inhibits the neuronal noradrenergic transporter.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
 KW Neurotoxin; Toxin; Hydroxylation.  
 FT DISULFID 2 11  
 FT DISULFID 3 8  
 FT MOD RES 10 10  
 FT MOD RES 11 10  
 QY SEQUENCE 11 AA; 1226 MW; 277AAC60B7232B58 CRC64;

Query Match 26.2%; Score 16; DB 1; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PC 11  
 DB 10 PC 11

RESULT 7  
 ID LPK2 LOCM1 STANDARD; PRT; 10 AA.  
 AC P41488;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Locustapyrokinin 2 (LOM-PK-2) (FXPRL-amide).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OX NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94094539; PubMed=7903606;  
 RA Schoofs L., Holman G.M., Nachman R., Proost P., van Damme J.,  
 RA de Loof A.;  
 RT "Isolation, identification and synthesis of locustapyrokinin II from  
 RT Locusta migratoria, another member of the FXPRL-amide peptide

RT family.";  
 RL Comp. Biochem. Physiol. 106C:103-109 (1993).  
 CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic  
 CC activity).  
 CC -!- SIMILARITY: Belongs to the pyrokinin family.  
 DR InterPro: IPR001484; PYROKININ.  
 DR PROSITE: PS00539; PYROKININ. 1.  
 KW Neuropeptide; Amidation; Pyrokinin; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 10 10 AMIDATION.  
 SQ SEQUENCE 10 AA; 1145 MW; CFAF4271A9D1B772 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 4.7e+03;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVP 5  
 DB 2 SVP 4

RESULT 8  
 ID AKH TABAT STANDARD; PRT; 8 AA.  
 AC P14595;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Adipokinetic hormone (AKH) (Dipteran corpora cardiaca factor I)  
 DE (DCC I).  
 OS Tabanus atratus (Horse fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
 OC Tabanus.  
 OX NCBI\_TaxID=7207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Corpora cardiaca;  
 RX MEDLINE=90046758; PubMed=2813385;  
 RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
 RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
 RT "Primary structure of two neuropeptide hormones with adipokinetic and  
 RT hypotrehalosemic activity isolated from the corpora cardiaca of horse  
 RT flies (Diptera)".  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164 (1989).  
 CC -!- FUNCTION: This hormone, released from cells in the corpora  
 CC cardiaca after the beginning of flight, causes release of  
 CC diglycerides from the fat body and then stimulates the flight  
 CC muscles to use these diglycerides as an energy source.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the AKH / HRTN / RPCH family.  
 DR PIR; A33995; A33995.  
 DR InterPro: IPR002047; AKH.  
 DR PROSITE: PS00256; AKH; 1.  
 KW Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
 FT MOD\_RES 8 8 AMIDATION.  
 SQ SEQUENCE 8 AA; 949 MW; 86786771A9D1A736 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LTSVP 10  
 DB 2 LTFTP 6

RESULT 9  
 ID HTF2 PERAM STANDARD; PRT; 8 AA.  
 AC P04549;  
 DT 13-AUG-1987 (Rel. 05, Created)

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DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrihaloaemic factor II (Neuropeptide M-II) (Periplaneta CC-2)
DE (Pea-CAH-II) (Leb-CC-II) (Hypertrihaloaemic neuropeptide II).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blattella orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 7539, 6976;
RN [1]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schaffer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry.";
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN [2]
RP SEQUENCE.
RC SPECIES=P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kalish F., Kramer S.J., McEnroe G.A.,
RA Miller C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN [3]
RP SEQUENCE.
RC SPECIES=L.decemlineata; TISSUE=Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiacum from the potato
RT beetle and the American cockroach are identical.";
RL Peptides 10:1287-1289(1989).
RN [4]
RP SEQUENCE.
RC SPECIES=B.orientalis; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrihaloaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blattella orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1- FUNCTION: Hypertrihaloaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR PIR; B44960; B44960.
DR PIR; B49823; B49823.
DR PIR; S08996; S08996.
DR InterPro; IPR02047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 8 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 1006 MW; 86745771A9D1A736 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 LTSPV 10
Db 2 LTTPP 6
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RESULT 10
UPAA_HUMAN
ID UPAA_HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 7, its MW is: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON_TER 1 1 F -> P.
FT VARIANT 5 5 /FTID=VAR_000004.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 23.0%; Score 14; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 VPLTSPV 10
Db 1 VILTFYP 7

RESULT 11
DNFI_LOCFI
ID DNFI_LOCFI STANDARD; PRT; 9 AA.
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locupressin (Diuretic neuropeptide F1/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN F1.
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).
FT MOD_RES 9 9 AMIDATION.
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SQ SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 LRSVP 10
DB 3 ITNCP 7

RESULT 12
YBFR_AZOVI
ID YBFR_AZOVI STANDARD; PRT; 9 AA.
AC P25825;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in bfr 3' region (Fragment).
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196129; PubMed=1549605;
RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,
RT Stiefel E.I.;
RL "Unification of the ferritin family of proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M83692; AAA22122.1; .
DR PIR; B41983;
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;

Query Match      23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTS 8
DB 4 PRTS 7

RESULT 13
BPP2_BOTJA
ID BPP2_BOTJA STANDARD; PRT; 10 AA.
AC P01022;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide 10B (Angiotensin-converting enzyme
DE inhibitor V-6-11).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RX TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sabo E.F., Pluscec J., Weaver E.R.,

us-09-761-636a-7.closed.rsp

RA Kocy O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RL Biochemistry 10:4033-4039(1971).
CC -!- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of the
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01255; XAVI6B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1
SQ SEQUENCE 10 AA; 1232 MW; 30C53546C7741773 CRC64;

Query Match      23.0%; Score 14; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.1e+03;
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 4 PRQIP 9

RESULT 14
HTF2_CARMO
ID HTF2_CARMO STANDARD; PRT; 10 AA.
AC P11385;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosaemic factor II (HTF-II) (HPTH-II) (Hypertrehalosaemic
DE neuroptide II).
OS Carausius morosus (Indian stick insect), and
OS Extatosoma tiaratum (Stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatodea;
OC Heteronemidae; Carausius.
OX NCBI_TaxID=7022, 7024;
RN [1]
RP SEQUENCE.
RX SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=87157103; PubMed=3828078;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structure of the hypertrehalosaemic factor II from the
RT corpus cardiaca of the Indian stick insect, Carausius morosus,
RT determined by fast atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN [2]
RP SEQUENCE.
RX SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry.";
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN [3]
RP CARBOHYDRATE-LINKAGE SITE.
RX SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX MEDLINE=93129188; PubMed=1482345;
RA Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT a stick insect corpus cardiaca.";
RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAH.
CC -!- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR PIR; JC1416; JC1416.
DR PIR; S09138; S09139.

```

DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1164 MW; 9B9036745771A9D1 CRC64;  
  
Query Match 23.0%; Score 14; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 LTSVP 10  
Db 2 LTFTP 6  
  
RESULT 15  
HTF\_TABAT STANDARD; PRT; 10 AA.  
AC P14596;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypertrehalosaemic factor (HOTH) (Dipteran corpora cardiaca factor II) (DCC II).  
OS Tabanus atratus (Horse fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;  
OC Tabanus.  
OX NCBI\_TaxID=7207;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Corpora cardiaca;  
RX MEDLINE=90046758; PubMed=2813385;  
RA Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,  
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;  
RT "Primary structure of two neuropeptide hormones with adipokinetic and  
RT hypotrehalosaemic activity isolated from the corpora cardiaca of horse  
RT flies (Diptera).";  
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).  
CC -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that  
CC elevate the level of trehalose in the hemolymph (trehalose is the  
CC major carbohydrate in the hemolymph of insects).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the AKH / HETH / RPCH family.  
DR PIR; B33995; B33995.  
DR InterPro; IPR002047; AKH.  
DR PROSITE; PS00256; AKH; 1.  
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT MOD\_RES 10 10 AMIDATION.  
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;  
  
Query Match 23.0%; Score 14; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 7.1e+03;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 6 LTSVP 10  
Db 2 LTFTP 6

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:43:34 ; Search time 58 Seconds  
(without alignments)  
59.840 Million cell updates/sec

Title: US-09-761-636A-7  
Perfect score: 61  
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1903

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_25.\*  
1: sp\_archaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_rvirus.\*  
16: sp\_bacteriaph.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	34.4	11	6 Q9TQSO	Q9tqs0 bos taurus
2	20	32.8	8	2 Q8GMMS	Q8gmms acinetobact
3	20	32.8	10	15 Q85598	Q85598 moloney mur
4	20	32.8	10	15 Q85563	Q85563 moloney mur
5	20	32.8	10	15 Q85619	Q85619 moloney mur
6	19	31.1	8	2 Q56140	Q56140 streptococ
7	19	31.1	10	8 Q9TKF7	Q9tkf7 agonis gran
8	19	31.1	10	8 Q9TKF9	Q9tkf9 melaleuca v
9	19	31.1	10	8 Q9TKG2	Q9tkg2 callistemon
10	19	31.1	10	8 Q9TKF1	Q9tkf1 homalospem
11	19	31.1	10	8 Q9TKF8	Q9tkf8 tristanlops
12	19	31.1	10	8 Q9TKF4	Q9tkf4 angasomyrtu
13	19	31.1	10	8 Q9TKF3	Q9tkf3 asteromyrtu
14	19	31.1	10	8 Q9TKE0	Q9tke0 neofabricia
15	19	31.1	10	8 Q9TKF0	Q9tkf0 kunzea ambi
16	19	31.1	10	8 Q9TKF6	Q9tkf6 agonis obtu

17	19	31.1	10	8 Q9THM7	Q9thm7 leptospermu
18	19	31.1	10	8 Q9TKE2	Q9tke2 leptospermu
19	19	31.1	10	8 Q9TKE3	Q9tke3 leptospermu
20	19	31.1	10	8 Q9TKE7	Q9tke7 kunzea pulc
21	19	31.1	10	8 Q9THM6	Q9thm6 leptospermu
22	19	31.1	10	8 Q9TKE6	Q9tke6 leptospermu
23	19	31.1	10	8 Q9TKE8	Q9tke8 kunzea eric
24	19	31.1	10	8 Q9TKE9	Q9tke9 kunzea baxt
25	19	31.1	10	8 Q9TKE1	Q9tke1 neofabricia
26	19	31.1	10	8 Q9TKE4	Q9tke4 leptospermu
27	19	31.1	10	8 Q9TKG0	Q9tkg0 lophostemon
28	19	31.1	11	10 P83092	P83092 spinacia ol
29	18	29.5	9	10 Q9FXL0	Q9fxl0 lilium long
30	18	29.5	11	4 Q9NYF38	Q9nyf38 homo sapien
31	18	29.5	11	11 Q99N81	Q99n81 mus musculu
32	17	27.9	8	2 Q8KPY4	Q8kpy4 microcystis
33	17	27.9	9	2 Q9K4M6	Q9k4m6 staphylococ
34	17	27.9	9	10 Q7X6A3	Q7x6a3 zea mays su
35	17	27.9	10	8 Q96041	Q96041 oenothera b
36	17	27.9	10	10 Q7Y0I8	Q7y0i8 zea mays su
37	17	27.9	10	12 Q39957	Q39957 hepatitis g
38	17	27.9	11	7 Q77872	Q77872 oreochromis
39	17	27.9	11	7 Q77873	Q77873 oreochromis
40	17	27.9	11	7 Q77871	Q77871 oreochromis
41	17	27.9	11	11 Q91Y49	Q91y49 mus musculu
42	16	26.2	8	2 Q849P4	Q849p4 salmonella
43	16	26.2	8	4 Q16468	Q16468 homo sapien
44	16	26.2	8	6 Q02831	Q02831 oryctolagus
45	16	26.2	8	6 Q9TRY3	Q9try3 sus sp. ins

#### ALIGNMENTS

RESULT 1  
Q9TQSO PRELIMINARY; PRT; 11 AA.  
AC Q9TQSO; 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)  
DE C-KIT (Fragment).  
GN KIT.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Olsen H.G., Vage D.I., Lien S., Klungland H.;  
RT "A polymorphism in the bovine c-kit gene."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ243424; CAB60775.1; --  
DR EMBL; AJ243060; CAB60774.1; --  
FT NON\_TER 1  
SQ SEQUENCE 11 AA; 1126 MW; DD785FF8A2D2D772 CRC64;

Query Match 34.4%; Score 21; DB 6; Length 11;  
Best Local Similarity 57.1%; Pred. No. 3.6e+03;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SVPLTSV 9  
:|:|:  
Db 3 AVPVSV 9

RESULT 2  
Q8GMMS PRELIMINARY; PRT; 8 AA.  
ID Q8GMMS  
AC Q8GMMS;  
DT 01-MAR-2003 (Tremblrel. 23, Created)

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DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Transposase (Fragment).
GN TNP17.
OS Acinetobacter sp. BW3.
OC Plasmid pKIH207.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=106395;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BM3; PLASMID=pKIH207;
RA Kholodii G.Y., Yuriyeva O.V., Mindlin S.Z., Gorlenko Z.M.,
RA Nikiforov V.G.;
RT "pKIH2-like aberrant transposons and possible mechanisms of their
RT dissemination.";
RN Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BM3; PLASMID=pKIH207;
RA Kholodii G.Y., Mindlin S.Z., Gorlenko Z.M., Yuriyeva O.V.,
RA Petrova M.A., Nikiforov V.G.;
RT "A young family of transposable adaptive DNA segments identified in
RT the Acinetobacter genus.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250234; CAC80784.1; -.
DR EMBL; AJ486856; CAD31078.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 911 MW; 2D71B2D6C1A73774 CRC64;

Query Match 32.8%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. NO. 1e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSV 9
Db 2 PLTQV 6

RESULT 3
Q85598 PRELIMINARY; PRT; 10 AA.
AC Q85598;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain HT1) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03106; AAA46492.1; -.
DR NON TER
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. NO. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 4
Q85563 PRELIMINARY; PRT; 10 AA.
AC Q85563;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Env-mos fusion protein (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=82196891; PubMed=6281735;
RA Donoghue D.J., Hunter T.;
RT "A generalized method of subcloning DNA fragments by restriction site
RT reconstruction: Application to sequencing the amino-terminal region of
RT the transforming gene of Gazdar murine sarcoma virus.";
RL Nucleic Acids Res. 10:2549-2564(1982).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03105; AAA46491.1; -.
DR NON TER
SQ SEQUENCE 10 AA; 1062 MW; F9ECFCBEA771B5B1 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. NO. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 5
Q85619 PRELIMINARY; PRT; 10 AA.
AC Q85619;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Moloney murine sarcoma virus (Strain ml) env/mos 5' junction
DE (Fragment).
OS Moloney murine leukemia virus.
OC Viruses; Retrovirdae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11801;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=83164305; PubMed=6300424;
RA Donoghue D.J., Hunter T.;
RT "Recombination junctions of variants of Moloney murine sarcom virus:
RT Generation and divergence of a mammalian transforming gene.";
RL J. Virol. 45:607-617(1983).
DR EMBL; K03108; AAA46494.1; -.
DR NON TER
SQ SEQUENCE 10 AA; 1081 MW; 7BECFCBEA771B5A4 CRC64;

Query Match 32.8%; Score 20; DB 15; Length 10;
Best Local Similarity 75.0%; Pred. NO. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 SVPC 11
Db 4 STPC 7

RESULT 6
Q56140

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ID Q56140 PRELIMINARY; PRT; 8 AA.  
 AC Q56140;  
 DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE STP6 protein (Fragment).  
 GN STP6.  
 OS Streptococcus thermophilus.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.  
 OX NCBI\_TaxID=1308;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Str11;  
 RX MEDLINE=95047254; PubMed=7958782;  
 RA Constable A., Mollet B.;  
 RT "Isolation and characterisation of promoter regions from Streptococcus  
 thermophilus". Lett. 122:85-90(1994).  
 RL FEMS Microbiol. Lett. 122:85-90(1994).  
 DR EMBL; X78210; CAA55045.1; -;  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 846 MW; ED086772D5B045B6 CRC64;  
 Query Match 31.1%; Score 19; DB 2; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ISVP 5  
 Db |||||  
 3 ISVP 6  
 RESULT 7  
 Q9TKF7 PRELIMINARY; PRT; 10 AA.  
 ID Q9TKF7  
 AC Q9TKF7;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE AtPB (Fragment).  
 GN AtPB.  
 OS Agonis grandiflora.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Myrtaceae; Agonis.  
 OX NCBI\_TaxID=106028;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;  
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";  
 RL Aust. J. Bot. 48:0-0(2000).  
 DR EMBL; AF184675; AAF03845.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;  
 Query Match 31.1%; Score 19; DB 8; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 PLTSVP 10  
 Db |||||  
 5 PTTSRP 10  
 RESULT 8  
 Q9TKF9 PRELIMINARY; PRT; 10 AA.  
 ID Q9TKF9  
 AC Q9TKF9;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DE AtPB (Fragment).  
 GN AtPB.

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE AtPB (Fragment).  
 GN AtPB.  
 OS Melaleuca viridiflora.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Myrtaceae; Melaleuca.  
 OX NCBI\_TaxID=106062;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;  
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";  
 RL Aust. J. Bot. 48:0-0(2000).  
 DR EMBL; AF184670; AAF03840.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1144 MW; 028C2CA1B1B76440 CRC64;  
 Query Match 31.1%; Score 19; DB 8; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 PLTSVP 10  
 Db |||||  
 5 PTTSRP 10  
 RESULT 9  
 Q9TKG2 PRELIMINARY; PRT; 10 AA.  
 ID Q9TKG2  
 AC Q9TKG2;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE AtPB (Fragment).  
 GN AtPB.  
 OS Callistemon polandii.  
 OG Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Myrtales; Myrtaceae; Callistemon.  
 OX NCBI\_TaxID=73732;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA O'Brien M.M., Quinn C.J., Wilson P.G.;  
 RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";  
 RL Aust. J. Bot. 48:0-0(2000).  
 DR EMBL; AF184666; AAF03836.1; -;  
 DR GO; GO:0009507; C:chloroplast; IEA.  
 KW Chloroplast.  
 FT NON TER 10  
 SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;  
 Query Match 31.1%; Score 19; DB 8; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 7.6e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 PLTSVP 10  
 Db |||||  
 5 PTTSRP 10  
 RESULT 10  
 Q9TKF1 PRELIMINARY; PRT; 10 AA.  
 ID Q9TKF1  
 AC Q9TKF1;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
 DE AtPB (Fragment).  
 GN AtPB.

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OS Homalospermum firmum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Homalospermum.
OX NCBI_TaxID=106039;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184682; AAF03852.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 11
Q9TKF8 PRELIMINARY; PRT; 10 AA.
AC Q9TKF8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN ATPB.
OS Tristaniopsis laurina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Tristaniopsis.
OX NCBI_TaxID=106073;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184672; AAF03842.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1126 MW; 15132CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 12
Q9TKF4 PRELIMINARY; PRT; 10 AA.
AC Q9TKF4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN ATPB.
OS Angasomyrtus salina.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Angasomyrtus.
OX NCBI_TaxID=106032;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184678; AAF03848.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 13
Q9TKF3 PRELIMINARY; PRT; 10 AA.
AC Q9TKF3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AtPB (Fragment).
GN ATPB.
OS Asteromyrtus brassii.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Asteromyrtus.
OX NCBI_TaxID=106034;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:621-628(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA O'Brien M.M., Quinn C.J., Wilson P.G.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Heslewood M., Quinn C.J.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF184679; AAF03849.2; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 5 PTTSRP 10

RESULT 14
Q9TKE0 PRELIMINARY; PRT; 10 AA.
AC Q9TKE0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```

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DE AtPB (Fragment).
GN ATPB.
OS Neofabricia sericisepala.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Neofabricia.
OX NCB1_TaxID=106065;
RN [1]
RP SEQUENCE FROM N.A.
RT O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184700; AAF03869.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db | | | |
5 FTTSRP 10

RESULT 15
Q9TKF0 PRELIMINARY; PRT; 10 AA.
AC Q9TKF0;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE AtPB (Fragment).
GN ATPB.
OS Kunzea ambigua (Tick bush).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Myrtales; Myrtaceae; Kunzea.
OX NCB1_TaxID=106041;
RN [1]
RP SEQUENCE FROM N.A.
RT O'Brien M.M., Quinn C.J., Wilson P.G.;
RT "Molecular Systematics of the Leptospermum Suballiance (Myrtaceae).";
RL Aust. J. Bot. 48:0-0(2000).
DR EMBL; AF184683; AAF03853.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 10 AA; 1172 MW; 1DB12CA1B1B76440 CRC64;

Query Match 31.1%; Score 19; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PLTSVP 10
Db | | | |
5 FTTSRP 10

Search completed: September 5, 2004, 10:47:58
Job time : 60 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:40:24 ; Search time 64 Seconds  
(without alignments)  
48.563 Million cell updates/sec

Title: US-09-761-636A-7

Perfect score: 61

Sequence: 1 CISVPLTSPVC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 348779

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	4	Aau04526
2	59	96.7	11	4	Aau04542
3	57	93.4	11	4	Aau04545
4	54	88.5	11	4	Aau04543
5	52	85.2	11	4	Aau04544
6	45.5	74.6	10	4	Aau04532
7	41	67.2	9	4	Aau04533
8	32	52.5	9	4	Aau04529
9	30	49.2	8	2	Aar58418
10	30	49.2	10	2	Aae34703
11	30	49.2	10	2	Aaw12561
12	29	47.5	11	5	Aaw12615
13	29	47.5	11	5	Abp47579
14	29	44.3	10	2	Abp47580
15	27	44.3	10	2	Aar77368
16	27	44.3	11	5	Abp47596
17	26	42.6	6	2	Aay41619
18	26	42.6	8	2	Aar58417
19	26	42.6	9	2	Aay26265
20	26	42.6	9	6	Abt56927
21	26	42.6	10	4	Aag73418
22	26	42.6	10	5	Abg64264
23	25.5	41.8	9	2	Aar96138
24	25.5	41.8	9	2	Aaw82212
25	25.5	41.8	9	2	Aaw46562

26 25 41.0 9 2 AAY26264 Isolated  
27 25 41.0 9 4 AAE01112 Human leu  
28 25 41.0 9 6 ABR24203 Human can  
29 25 41.0 9 6 AAE29971 Human air  
30 25 41.0 10 2 AAW01720 Inhibitor  
31 25 41.0 10 2 AAR90487 Antibody  
32 25 41.0 10 2 AAW88078 Inhibitor  
33 25 41.0 10 2 AAY55214 Anti CD34  
34 25 41.0 10 3 AAY86960 Human hae  
35 25 41.0 10 3 AAY77429 Fibronect  
36 25 41.0 10 4 AAG95853 Human com  
37 25 41.0 10 6 ABR24101 Human can  
38 25 41.0 10 6 ABR24325 Human can  
39 25 41.0 10 6 ABR24347 Human can  
40 25 41.0 11 4 AAU00642 Human mem  
41 25 41.0 11 7 ADB88785 Membrane  
42 24 39.3 6 2 AAR03869 Hypotensi  
43 24 39.3 6 4 AAE05003 Human rel  
44 24 39.3 6 4 AAB60620 Human MMW  
45 24 39.3 7 4 AAU04530 VEGF base

## ALIGNMENTS

RESULT 1  
AAU04526  
ID AAU04526 standard; peptide; 11 AA.  
XX AC AAU04526;  
XX XX  
DT 26-SEP-2001 (first entry)  
XX XX  
DE VEGF based monocyclic peptide 3.  
XX XX  
KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.  
XX OS Synthetic.  
XX XX  
FH Key Location/Qualifiers  
FT Disulfide-bond 1..11  
FT FT  
XX XX  
PN WO200152875-A1.  
XX XX  
PD 26-JUL-2001.  
XX XX  
PF 18-JAN-2001; 2001WO-US001533.  
XX XX  
PR 18-JAN-2000; 2000US-0176293P.  
PR 16-MAY-2000; 2000US-0204590P.  
XX XX  
PA (LUDW-) LUDWIG INST CANCER RES.  
XX XX  
PI Achen MG, Hughes RA, Stacker S, Cendron A;  
XX XX  
XX WPI; 2001-442248/47.  
XX XX  
PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
PT residues.  
XX XX  
PS Claim 49; Page 32; 102pp; English.  
XX XX  
CC The sequence represents a monomeric monocyclic peptide of the invention,  
CC whose 3-dimensional structure is modelled on the exposed loop of human  
CC VEGF (vascular endothelial growth factor). The invention relates to a  
CC method of producing a monomeric monocyclic peptide by a measuring beta-  
CC beta carbon separation distances on opposite antiparallel strands of a

/note= "This bond cyclises the peptide"

CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 CC  
 XX SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 4; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 0.0016;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CTSVPLTSPVC 11  
 |||||  
 Db 1 CTSVPLTSPVC 11

RESULT 2  
 AAU04542  
 ID AAU04542 standard; peptide; 11 AA.  
 XX AC AAU04542;  
 XX 26-SEP-2001 (first entry)  
 DT VEGF based monocyclic peptide 20.  
 DE  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1. .11  
 FT /note= "This bond cyclises the peptide"  
 XX  
 XX WO200152875-A1.  
 PN  
 XX 26-JUL-2001.  
 PD  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 PR  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX WPI; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT

PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 XX  
 CC The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 CC  
 XX SQ Sequence 11 AA;

Query Match 96.7%; Score 59; DB 4; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.0034;  
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTSVPLTSPVC 11  
 |||||  
 Db 1 CTSVPLTSPVC 11

RESULT 3  
 AAU04545  
 ID AAU04545 standard; peptide; 11 AA.  
 XX AC AAU04545;  
 XX 26-SEP-2001 (first entry)  
 DT VEGF based monocyclic peptide 23.  
 DE  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1. .11  
 FT /note= "This bond cyclises the peptide"  
 XX  
 XX WO200152875-A1.  
 PN  
 XX 26-JUL-2001.  
 PD  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 PR  
 XX

PA (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX  
 XX Example 25; Page 47; 102pp; English.  
 XX  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 11 AA;  
 Query Match 93.4%; Score 57; DB 4; Length 11;  
 Best Local Similarity 81.8%; Pred. No. 0.0072;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CISVPLTSVPC 11  
 |:|||||:  
 Db 1 CVSPLTTVPC 11  
 RESULT 4  
 AAU04543  
 ID AAU04543 standard; peptide; 11 AA.  
 XX  
 AC AAU04543;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based monocyclic peptide 21.  
 XX  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH Disulfide-bond 1..11  
 FT /note= "This bond cyclises the peptide"  
 FT  
 XX

PN WO200152875-A1.  
 XX 26-JUL-2001.  
 PD  
 XX 18-JAN-2001; 2001WO-US001533.  
 PF  
 XX 18-JAN-2000; 2000US-0176293p.  
 PR  
 PR 16-MAY-2000; 2000US-0204590p.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX  
 XX Example 25; Page 47; 102pp; English.  
 PS  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 11 AA;  
 Query Match 88.5%; Score 54; DB 4; Length 11;  
 Best Local Similarity 72.7%; Pred. No. 0.023;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CISVPLTSVPC 11  
 |:|||||:  
 Db 1 CITIPLTSLPC 11  
 RESULT 5  
 AAU04544  
 ID AAU04544 standard; peptide; 11 AA.  
 XX  
 AC AAU04544;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based monocyclic peptide 22.  
 XX  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 XX  
 OS Synthetic.

XX Key Location/Qualifiers  
 XX Disulfide-bond 1..11  
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.  
 XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stackler S, Cendron A;  
 PI WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.

XX Example 25; Page 47; 102pp; English.  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 XX whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX

XX Sequence 11 AA;

Query Match 85.2%; Score 52; DB 4; Length 11;  
 Best Local Similarity 72.7%; Pred. No. 0.049;  
 Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CISVPLTSVPC 11  
 |||:|:|:|  
 Db 1 CISLPISSVPC 11

RESULT 6  
 AAU04532  
 ID AAU04532 standard; peptide; 10 AA.

XX  
 AC  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based monocyclic peptide 10.  
 XX  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FT Disulfide-bond 1..10  
 FT /note= "This bond cyclises the peptide"  
 XX  
 XX WO200152875-A1.  
 XX 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stackler S, Cendron A;  
 PI WPI; 2001-442248/47.  
 DR Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 PT  
 XX Claim 49; Page 32; 102pp; English.  
 PS The sequence represents a monomeric monocyclic peptide of the invention,  
 XX whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 XX Sequence 10 AA;

Query Match 74.6%; Score 45.5; DB 4; Length 10;  
 Best Local Similarity 90.9%; Pred. No. 0.52;  
 Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;



QY 1 CISVPLTSVPC 11  
 ||||| |||||  
 Db 1 CISVPL-SVPC 10

## RESULT 7

AAU04533  
 ID AAU04533 standard; peptide; 9 AA.

AC AAU04533;

DT 26-SEP-2001 (first entry)

VEGF based monocyclic peptide 11.

Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 diabetes induced neovascular sequelae; rheumatoid arthritis;  
 diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and

CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy

SQ Sequence 9 AA;

Query Match 67.2%; Score 41; DB 4; Length 9;

Best Local Similarity 81.8%; Pred No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPLTSVPC 11

||||| |||||

Db 1 CISVPL--VPC 9

## RESULT 8

AAU04529

ID AAU04529 standard; peptide; 9 AA.

AC AAU04529;

DT 26-SEP-2001 (first entry)

VEGF based monocyclic peptide 7.

Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 diabetes induced neovascular sequelae; rheumatoid arthritis;  
 diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 1..9 /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.

XX Claim 49; Page 32; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold

CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ

Sequence 9 AA;

Query Match 52.5%; Score 32; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9  
 Db 2 SVPLTSV 8  
 |||||

RESULT 9  
 AAR58418  
 ID AAR58418 standard; protein; 8 AA.

XX AAR58418;

AC  
 XX 25-MAR-2003 (revised)  
 DT 13-APR-1995 (first entry)

XX Partial peptide 7 from TSAR C46.9-2 binding domain.

XX TSAR; totally synthetic affinity reagent; synthetic; binding domain;  
 KW effector domain; concatenated heterofunctional protein; linker; direct;  
 KW rapid; detection; screening; treatment; monoclonal antibody; MAb; C46;  
 KW anti-carcinoembryonic antigen; anti-CEA.

OS Synthetic.

XX WO9418318-A1.

XX 18-AUG-1994.

XX 01-FEB-1994; 94WO-US000977.

XX 01-FEB-1993; 93US-00013416.

PR 30-DEC-1993; 93US-00176500.

PR 31-JAN-1994; 94US-00189331.

XX (UYN-) UNIV NORTH CAROLINA.

XX Kay EK, Fowlkes DW;

XX WPI; 1994-279739/34.

XX Identifying proteins or peptide(s) which bind a ligand - by screening a  
 PT recombinant vector library expressing fusion proteins comprising a  
 PT binding domain and an effector domain.

XX Example 7.5; Page 108; 255pp; English.

XX AAR58412-42 are overlapping 8-mer peptides of the binding domain of TSAR  
 CC (Totally Synthetic Affinity Reagents) peptide TSAR C46.9-2 (AAR58411).  
 CC These bind (partially) a monoclonal antibody, ie. anti-CEA C46 (anti  
 CC carcinoembryonic antigen). TSAR peptides are generated using generic  
 CC oligonucleotides (see AAQ07470-73 for examples). TSARs are concatenated  
 CC heterofunctional proteins or peptides, comprising at least two functional  
 CC regions - a binding domain with affinity for a ligand and a second  
 CC effector peptide portion that is chemically or biologically active. They  
 CC may further comprise a linker peptide between the 2 domains. The TSARs or

CC compens. comprising a TSAR binding domain can be used in vivo to deliver  
 CC a chemically or biologically active moiety, eg. metal ion, radioisotope,  
 CC peptide, toxin or enzyme, to the specific target or on the cell. They can  
 CC also replace the function of macromolecules eg. monoclonal or polyclonal  
 CC antibodies and therefore circumvent the need for complex methods of  
 CC hybridoma formation or in vivo antibody production. The TSARs are easily  
 CC characterised and have designed activity allowing direct and rapid  
 CC detection in a screening process. (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX

SQ Sequence 8 AA;

Query Match 49.2%; Score 30; DB 2; Length 8;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTSVPLTS 8  
 Db 1 CVSAPQTS 8  
 :|||

RESULT 10  
 AAE34703  
 ID AAE34703 standard; peptide; 9 AA.

XX AAE34703;

XX 14-MAY-2003 (first entry)

XX CA125/MUC16 O-glycosylation site #1.

XX CA125; antigen; cancer; gene therapy; vaccine; MUC16.

XX Unidentified.

XX WO200292836-A2.

XX 21-NOV-2002.

XX 09-MAY-2002; 2002WO-US014768.

XX 11-MAY-2001; 2001US-0290480P.

XX (SLOK ) SLOAN KETTERING INST CANCER RES.

XX Lloyd KO, Yin BWT;

XX WPI; 2003-129305/12.

XX New isolated nucleic acid molecule comprising sequences encoding the  
 PT CA125 protein, useful for diagnosing, preventing and/or treating cancer,  
 PT e.g. ovarian, pancreatic, breast, endometrial or lung carcinomas.

XX Disclosure; Page 19; 70pp; English.

XX The invention relates to a nucleic acid molecule encoding an ovarian  
 CC cancer antigen, CA125. Nucleic acid molecules, vaccine and methods are  
 CC useful for diagnosing, preventing and treating cancer, e.g. pancreatic,  
 CC lung, ovarian, breast or endometrial carcinoma. The invention is useful  
 CC in gene therapy and as vaccines. The present sequence is CA125/MUC16 O-  
 CC glycosylation site  
 XX

SQ Sequence 9 AA;

Query Match 49.2%; Score 30; DB 6; Length 9;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 SVPLTSVP 10  
 Db 2 SVPTTSTP 9  
 |||||

## RESULT 11

AAW12561  
ID AAW12561 standard; peptide; 10 AA.  
XX  
AC AAW12561;  
XX  
DT 08-APR-1997 (first entry)  
XX  
DE SH2 binding peptide core sequence #11.  
XX  
KW Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes;  
KW insulin-resistant diabetes.  
XX  
OS Synthetic.  
XX  
FN Key Location/Qualifiers  
FT Modified-site 3 /label= OTHER  
FT /notes="Given in the patent as PI, no further details given. May be intended to be phosphoryrosine"  
FT  
XX  
PN WO9623813-A1.  
XX  
PD 08-AUG-1996.  
XX  
PF 31-JAN-1996; 96WO-US001544.  
XX  
PR 01-FEB-1995; 95US-00382100.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;  
PI Szardenings AK;  
XX  
DR WPI; 1996-371373/37.  
XX  
PT Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.  
XX  
PS Claim 8; Page 116; 203pp; English.  
XX

The sequences given in AAW12551-70 represent core peptides of an src homology region 2 (SH2) binding peptide which correspond to the formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its isostere; and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphoryrosine and Z8 is acylated, then the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphoryrosine and Z8 is asparagine, then the peptide is not GGGZ7XZ8XPLLL. SH2 binding peptides containing these core peptides are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes

Sequence 10 AA;

Query Match 49.2%; Score 30; DB 2; Length 10;  
Best Local Similarity 71.4%; Pred. NO. 1.9e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVPLT 7  
Db 2 C1NVPFT 8

## RESULT 12

AAW12615  
ID AAW12615 standard; peptide; 11 AA.  
XX

AAW12615;  
XX  
DT 08-APR-1997 (first entry)  
XX  
DE SH2 binding peptide core sequence #21.  
XX  
KW Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes;  
KW insulin-resistant diabetes.  
XX  
OS Synthetic.  
XX  
PN WO9623813-A1.  
XX  
PD 08-AUG-1996.  
XX  
PF 31-JAN-1996; 96WO-US001544.  
XX  
PR 01-FEB-1995; 95US-00382100.  
XX  
PA (AFFY-) AFFYMAX TECHNOLOGIES NV.  
XX  
PI Patel DV, Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH;  
PI Szardenings AK;  
XX  
DR WPI; 1996-371373/37.  
XX  
PT Peptide(s) which bind to SH2 domains - are used to treat diseases associated with aberrant cell growth, differentiation or regulation associated with defects in receptor tyrosine kinase pathways.  
XX  
PS Claim 13; Page 117; 203pp; English.

This sequence represents a core peptide of an src homology region 2 (SH2) binding peptide corresponding to the formula: Z7-X-Z8-X X = any D- or L- amino acid; Z7 = phosphotyrosine or its isostere; Z8 = asparagine or its isostere; the amino terminus is acylated, and the peptide is less than 14 residues in length, with the proviso that if Z7 is phosphoryrosine and Z8 is asparagine, then the peptide is not GGGZ7XZ8XPLLL. SH2 binding peptides containing this core peptide are used to treat of diagnose diseases associated with aberrant cell growth, differentiation or regulation which is associated with defects in receptor tyrosine kinase pathways, by partially blocking or inhibiting a cellular signal transduction pathway. The disease may be cancer, a developmental or differentiation disease or insulin-resistant (or non-insulin dependent) diabetes

Sequence 11 AA;

Query Match 49.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 71.4%; Pred. NO. 2.1e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 C1SVPLT 7  
Db 2 C1NVPFT 8

## RESULT 13

ABP47579  
ID ABP47579 standard; peptide; 11 AA.  
XX

AC ABP47579;

DT 19-AUG-2002 (first entry)

DE N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:155.  
XX  
KW Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS;  
KW lipooligosaccharide; monoclonal antibody; antibacterial; infection;  
KW antiinflammatory; meningococcal disease.  
XX

```

OS Neisseria meningitidis.
OS Synthetic.
XX
XX PN WO200228888-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 03-OCT-2001; 2001WO-EP011409.
XX
XX PR 03-OCT-2000; 2000GB-00024200.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI De Bolle XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
XX WPI; 2002-479596/51.
XX
XX PT Novel mimotope of Neisseria meningitidis surface, for treating
XX meningococcal disease, comprising a peptide epitope obtainable by
XX screening peptide library with a specific monoclonal antibody.
XX
XX PS Claim 15; Page 43; 55pp; English.
XX
XX CC The present invention describes mimotopes (I) of a surface L3, 7, 9, of
XX meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
XX comprising a peptide epitope obtained by screening a peptide library with
XX a monoclonal antibody (MAB) like 4BE12C10, H44/24, H44/58, H44/70 or
XX H44/78. (I) is antigenically cross-reactive with MAB. (I) have
XX antibacterial and antiinflammatory activities, and can be used in
XX vaccines. MAB is useful in the identification of (I). (I) or MAB are
XX useful as a medicament, and also in the manufacture of a medicament for
XX treating or preventing meningococcal disease. (I) and MAB are useful for
XX treating a patient suffering from or susceptible to meningococcal disease
XX by administering (I) or MAB to the patient. (I) is useful in a diagnostic
XX assay for meningococcal infection to detect antibodies against L3, 7, 9,
XX LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a
XX sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754
XX represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 47.5%; Score 29; DB 5; Length 11;
XX Best Local Similarity 27.3%; Pred. No. 3.1e+02;
XX Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CTSVPLTSVPC 11
XX |::|
XX 1 CWTIPYRGTC 11
XX
XX Db
XX
XX RESULT 14
XX ABP47580
XX ID ABP47580 standard; peptide; 11 AA.
XX
XX AC ABP47580;
XX
XX XX 19-AUG-2002 (first entry)
XX
XX DE N. meningitidis LOS peptidic mimotope related peptide SEQ ID NO:156.
XX
XX KW Neisseria meningitidis; meningococcus; meningococcal; vaccine; LOS;
XX KW lipooligosaccharide; monoclonal antibody; antibacterial; infection;
XX KW antiinflammatory; meningococcal disease.
XX
XX OS Neisseria meningitidis.
XX OS Synthetic.
XX
XX PN WO200228888-A2.
XX
XX PD 11-APR-2002.
XX
XX PF 03-OCT-2001; 2001WO-EP011409.
XX
XX PR 03-OCT-2000; 2000GB-00024200.
XX
XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX PI De Bolle XT, Letesson J, Lobet Y, Mertens PY, Poolman J, Voet P;
XX WPI; 2002-479596/51.
XX
XX PT Novel mimotope of Neisseria meningitidis surface, for treating
XX meningococcal disease, comprising a peptide epitope obtainable by
XX screening peptide library with a specific monoclonal antibody.
XX
XX PS Claim 15; Page 43; 55pp; English.
XX
XX CC The present invention describes mimotopes (I) of a surface L3, 7, 9, of
XX meningococcal lipopolysaccharides (LOS) of Neisseria meningitidis
XX comprising a peptide epitope obtained by screening a peptide library with
XX a monoclonal antibody (MAB) like 4BE12C10, H44/24, H44/58, H44/70 or
XX H44/78. (I) is antigenically cross-reactive with MAB. (I) have
XX antibacterial and antiinflammatory activities, and can be used in
XX vaccines. MAB is useful in the identification of (I). (I) or MAB are
XX useful as a medicament, and also in the manufacture of a medicament for
XX treating or preventing meningococcal disease. (I) and MAB are useful for
XX treating a patient suffering from or susceptible to meningococcal disease
XX by administering (I) or MAB to the patient. (I) is useful in a diagnostic
XX assay for meningococcal infection to detect antibodies against L3, 7, 9,
XX LOS and to detect the presence of L3, 7, 9 immunotype meningococcus in a
XX sample from a patient. ABN88464 to ABN88487 and ABP47336 to ABP47754
XX represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 11 AA;
XX
XX Query Match 47.5%; Score 29; DB 5; Length 11;
XX Best Local Similarity 27.3%; Pred. No. 3.1e+02;
XX Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX
XX QY 1 CTSVPLTSVPC 11
XX |::|
XX 1 CWTIPYRGTC 11
XX
XX Db
XX
XX RESULT 15
XX AAR77368
XX ID AAR77368 standard; peptide; 10 AA.
XX
XX AC AAR77368;
XX
XX XX 17-JAN-1996 (first entry)
XX
XX DE SH3 binding domain CAIR-1 B.
XX
XX KW Carboxyamido-triazole resistance; CAI; CAIR-1; cancer; gene therapy;
XX KW Src homology 3; SH3 binding domain.
XX
XX OS Homo sapiens.
XX
XX PN WO9525125-A1.
XX
XX PD 21-SEP-1995.
XX
XX PF 14-MAR-1995; 95WO-US003610.
XX
XX PR 14-MAR-1994; 94US-00212190.
XX
XX XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PA Kohn EC, Liotta LA, Kim YS;
XX PI WPI; 1995-336944/43.
XX
XX DR DNA encoding CAI resistance proteins - used in gene therapy, and for
XX PT detecting CAI resistance in biological samples.
XX

```

PS Example 4; Page 40; 56pp; English.  
XX  
CC CAIR-1 protein (AAR77365), responsible for CAI resistance in A2058 human  
CC melanoma cells, contains a unique proline-rich sequence which fulfills  
CC the consensus definition for Src homology 3 (SH3) binding proteins  
CC (AAR77366). 4 Unique versions (AAR77367-70) are present  
XX  
SQ Sequence 10 AA;  
Query Match 44.3%; Score 27; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4 VPLTSVPC 11  
Db 1 VPPAPVPC 8

Search completed: September 5, 2004, 10:46:32  
Job time : 66 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:46:55 ; Search time 67 Seconds  
(without alignments)  
51.727 Million cell updates/sec

Title: US-09-761-636A-7  
Perfect score: 61  
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 171292

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	100.0	11	9	US-09-761-636A-7
2	59	96.7	11	9	US-09-761-636A-23
3	57	93.4	11	9	US-09-761-636A-26
4	54	88.5	11	9	US-09-761-636A-24
5	52	85.2	11	9	US-09-761-636A-25
6	45.5	74.6	10	9	US-09-761-636A-13
7	41	67.2	9	9	US-09-761-636A-10
8	32	52.5	9	9	US-09-761-636A-14
9	29	47.5	9	12	US-10-253-286-332
10	29	47.5	9	15	US-10-245-871-332
11	29	47.5	11	12	US-10-398-104-155
12	29	47.5	11	12	US-10-398-104-156
13	29	47.5	11	14	US-10-126-845-89
14	28	45.9	9	15	US-10-154-884B-11221
15	27	44.3	9	15	US-10-154-884B-11228

16	27	44.3	9	15	US-10-154-884B-11250	Sequence 11250, A
17	27	44.3	9	15	US-10-154-884B-11254	Sequence 11254, A
18	27	44.3	9	15	US-10-154-884B-11258	Sequence 11258, A
19	27	44.3	9	15	US-10-154-884B-11259	Sequence 11259, A
20	27	44.3	9	15	US-10-154-884B-11265	Sequence 11265, A
21	27	44.3	9	15	US-10-154-884B-11275	Sequence 11275, A
22	27	44.3	9	15	US-10-154-884B-11280	Sequence 11280, A
23	27	44.3	11	12	US-10-398-104-172	Sequence 172, App
24	26	42.6	9	13	US-10-066-151-20	Sequence 20, Appl
25	26	42.6	9	13	US-10-358-052-20	Sequence 20, Appl
26	26	42.6	10	11	US-09-833-245-1011	Sequence 1011, Ap
27	25	41.0	9	13	US-10-066-151-19	Sequence 19, Appl
28	25	41.0	9	15	US-10-358-052-19	Sequence 19, Appl
29	25	41.0	9	15	US-10-358-052-52	Sequence 52, Appl
30	25	41.0	9	16	US-10-471-895-10	Sequence 10, Appl
31	25	41.0	10	10	US-09-572-404B-2047	Sequence 2047, Ap
32	25	41.0	11	14	US-10-126-845-12	Sequence 12, Appl
33	25	41.0	11	14	US-10-126-845-70	Sequence 70, Appl
34	25	41.0	11	15	US-10-116-275-100	Sequence 100, App
35	25	41.0	11	16	US-10-784-235-12	Sequence 12, Appl
36	24	39.3	5	9	US-09-886-135-5	Sequence 5, Appli
37	24	39.3	5	10	US-09-886-135-5	Sequence 5, Appli
38	24	39.3	7	9	US-09-761-636A-11	Sequence 11, Appl
39	24	39.3	7	12	US-10-620-278-19	Sequence 19, Appl
40	24	39.3	7	14	US-10-220-033-28	Sequence 28, Appl
41	24	39.3	9	12	US-09-935-430-249	Sequence 249, App
42	24	39.3	9	12	US-09-935-430-322	Sequence 322, App
43	24	39.3	9	12	US-09-935-430-349	Sequence 349, App
44	24	39.3	9	12	US-09-935-430-464	Sequence 464, App
45	24	39.3	9	13	US-10-066-151-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1  
US-09-761-636A-7  
; Sequence 7, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761.636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-636A-7

Query Match 100.0%; Score 61; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0036;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CISVPLTSVPC 11  
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Db 1 CISVPLTSVPC 11

RESULT 2  
US-09-761-636A-23  
; Sequence 23, Application US/09761636A  
; Patent No. US20020065218A1

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-23

Query Match          96.7%; Score 59; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0074;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 C1SVPLTSVPC 11

RESULT 3
US-09-761-636A-26
; Sequence 26, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 26
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-26

Query Match          93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.015;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 C1SVPLTSVPC 11

RESULT 4
US-09-761-636A-24
; Sequence 24, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match          85.2%; Score 52; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.095;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 C1SVPLTSVPC 11

RESULT 5
US-09-761-636A-25
; Sequence 25, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 25
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-25

Query Match          88.5%; Score 54; DB 9; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.046;
Matches 8; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 C1SVPLTSVPC 11

RESULT 6
US-09-761-636A-13
; Sequence 13, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 11
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-24
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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-13

Query Match      74.6%; Score 45.5; DB 9; Length 10;
Best Local Similarity 90.9%; Pred. No. 0.93;
Matches 10; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 CISVPLTSVPC 11
Db 1 CISVPL-SVPC 10

RESULT 7
US-09-761-636A-14
; Sequence 14, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-14

Query Match      67.2%; Score 41; DB 9; Length 9;
Best Local Similarity 81.8%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 CISVPLTSVPC 11
Db 1 CISVPL--VPC 9

RESULT 8
US-09-761-636A-10
; Sequence 10, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-10

Query Match      52.5%; Score 32; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SVPLTSV 9
Db 2 SVPLTSV 8

RESULT 9
US-10-253-286-332
; Sequence 332, Application US/10253286
; Publication No. US20040058881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2015
; CURRENT APPLICATION NUMBER: US/10/253,286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-332

Query Match      47.5%; Score 29; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPLTSVP 10
Db 2 VPIITSP 8

RESULT 10
US-10-245-871-332
; Sequence 332, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I1-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 332
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-245-871-332

Query Match      47.5%; Score 29; DB 15; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Query Match 47.5%; Score 29; DB 12; Length 11;
Best Local Similarity 36.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 CFAPPYDPLPC 11

RESULT 11
US-10-398-104-155
; Sequence 155, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-155

Query Match 47.5%; Score 29; DB 12; Length 11;
Best Local Similarity 27.3%; Pred. No. 4.2e+02;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 CVTIPYRGTC 11

RESULT 12
US-10-398-104-156
; Sequence 156, Application US/10398104
; Publication No. US20040047880A1
; GENERAL INFORMATION:
; APPLICANT: De Bolle, Xavier Thomas
; APPLICANT: Letesson, Jean-Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Mertens, Pascal Yvon
; APPLICANT: Poolman, Jan
; APPLICANT: Voet, Pierre
; TITLE OF INVENTION: COMPONENT FOR VACCINE
; FILE REFERENCE: B45242
; CURRENT APPLICATION NUMBER: US/10/398,104
; CURRENT FILING DATE: 2003-01-04
; PRIOR APPLICATION NUMBER: PCT/EP01/11409
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: GB 0024200.8
; PRIOR FILING DATE: 2000-10-03
; NUMBER OF SEQ ID NOS: 352
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LOS peptide mimotope sequence
US-10-398-104-156

Query Match 47.5%; Score 29; DB 12; Length 11;
Best Local Similarity 36.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 CFAPPYDPLPC 11

RESULT 13
US-10-126-845-89
; Sequence 89, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Pinilla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126,845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 89
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form peptide
; NAME/KEY: MISC FEATURE
; LOCATION: (1)-(11)
; OTHER INFORMATION: D form retroinversion peptide
US-10-126-845-89

Query Match 47.5%; Score 29; DB 14; Length 11;
Best Local Similarity 45.5%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 C1SVPLTSVPC 11
Db 1 CLLVPLLVAC 11

RESULT 14
US-10-154-884B-11221
; Sequence 11221, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
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; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11221
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-884B-11221

Query Match          45.9%; Score 28; DB 15; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CUSVPL 7
Db 2 CLSVPVS 8

RESULT 15
US-10-154-884B-11228
; Sequence 11228, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; TITLE OF INVENTION: Hematological Malignancies
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11228
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-154-884B-11228

Query Match          44.3%; Score 27; DB 15; Length 9;
Best Local Similarity 56.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CUSVPL 6  
Db 4 CLSVPV 9

Search completed: September 5, 2004, 10:52:48  
Job time : 67 secs

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**uspto**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:45:30 ; Search time 20 Seconds  
(without alignments)  
28.394 Million cell updates/sec

Title: US-09-761-636A-7  
Perfect score: 61  
Sequence: 1 CISVPLTSVPC 11

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 112282

Minimum DB seq length: 0  
Maximum DB seq length: 11

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	49.2	8	1 US-08-189-331-150	Sequence 150, App
2	30	49.2	8	2 US-08-471-068-150	Sequence 150, App
3	27	44.3	10	1 US-08-212-190A-5	Sequence 5, Appl
4	27	44.3	10	2 US-08-900-321-5	Sequence 5, Appl
5	27	44.3	10	5 PCT-US95-03610-5	Sequence 5, Appl
6	26	42.6	6	2 US-08-769-745-15	Sequence 15, Appl
7	26	42.6	8	1 US-08-189-331-149	Sequence 149, App
8	26	42.6	8	2 US-08-471-068-149	Sequence 149, App
9	25.5	41.8	9	1 US-08-331-383-33	Sequence 33, Appl
10	25.5	41.8	9	1 US-08-549-008-43	Sequence 43, Appl
11	25.5	41.8	9	3 US-08-802-981-143	Sequence 143, App
12	25	41.0	8	1 US-08-360-239B-1	Sequence 1, Appl
13	25	41.0	10	2 US-08-483-077C-26	Sequence 26, Appl
14	25	41.0	10	2 US-08-519-109B-26	Sequence 26, Appl
15	25	41.0	10	2 US-08-482-228-108	Sequence 108, App
16	25	41.0	10	3 US-08-482-528-108	Sequence 108, App
17	25	41.0	10	5 PCT-US95-10811-38	Sequence 38, Appl
18	24	39.3	6	1 US-08-483-434A-21	Sequence 21, Appl
19	24	39.3	6	3 US-08-476-134A-30	Sequence 30, Appl
20	24	39.3	6	6 5190920-26	Patent No. 5190920
21	24	39.3	6	6 5506208-28	Patent No. 5506208
22	24	39.3	7	4 US-09-438-150-1	Sequence 1, Appl
23	24	39.3	9	2 US-08-340-283-154	Sequence 154, App
24	24	39.3	9	4 US-09-601-729-204	Sequence 204, App
25	24	39.3	10	3 US-08-836-075A-187	Sequence 187, App
26	23.5	38.5	9	1 US-08-331-383-31	Sequence 31, Appl
27	23.5	38.5	9	1 US-08-549-008-42	Sequence 42, Appl

28 23.5 38.5 9 3 US-08-802-981-142 Sequence 142, App  
29 23.5 38.5 11 3 US-08-802-981-144 Sequence 144, App  
30 23 37.7 8 1 US-08-189-331-147 Sequence 147, App  
31 23 37.7 8 1 US-08-189-331-148 Sequence 148, App  
32 23 37.7 8 2 US-08-340-283-61 Sequence 61, Appl  
33 23 37.7 8 2 US-08-471-068-147 Sequence 147, App  
34 23 37.7 8 2 US-08-471-068-148 Sequence 148, App  
35 23 37.7 9 1 US-08-193-075-4 Sequence 4, Appl  
36 23 37.7 9 1 US-08-467-083-3 Sequence 3, Appl  
37 23 37.7 9 1 US-08-414-417B-3 Sequence 3, Appl  
38 23 37.7 9 2 US-08-486-348A-3 Sequence 3, Appl  
39 23 37.7 9 2 US-08-468-545B-3 Sequence 3, Appl  
40 23 37.7 9 3 US-08-466-680B-3 Sequence 3, Appl  
41 23 37.7 9 4 US-08-403-459-25 Sequence 25, Appl  
42 23 37.7 9 4 US-09-997-579-19 Sequence 19, Appl  
43 23 37.7 9 4 US-09-354-533-3 Sequence 3, Appl  
44 23 37.7 9 5 PCT-US95-01672-4 Sequence 4, Appl  
45 23 37.7 10 1 US-08-033-857A-5 Sequence 5, Appl

## ALIGNMENTS

RESULT 1  
US-08-189-331-150  
; Sequence 150, Application US/08189331  
; Patent No. 5747334  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 186  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189,331  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 150:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-189-331-150

Query Match 49.2%; Score 30; DB 1; Length 8;  
Best Local Similarity 62.5%; Pred. No. 3e+05;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CISVPLTS 8

Db 1 CVSAPQTS 8

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RESULT 2
US-08-471-068-150
; Sequence 150, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowlkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 150:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-068-150

Query Match 49.2%; Score 30; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLTS 8
Db 1 C1SAPQTS 8

RESULT 3
US-08-212-190A-5
; Sequence 5, Application US/08212190A
; Patent No. 5652223
; GENERAL INFORMATION:
; APPLICANT: KOHN, Elise C.
; APPLICANT: LIOTTA, Lance A.
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/212,190A
; FILING DATE: 14-MAR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 15280-204US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-190A-5

Query Match 44.3%; Score 27; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11
Db 1 VPPAPVPC 8

RESULT 4
US-08-900-321-5
; Sequence 5, Application US/08900321
; Patent No. 5981712
; GENERAL INFORMATION:
; APPLICANT: Kohn, Elise C.
; APPLICANT: Liotta, Lance A.
; APPLICANT: Kim, Young S.
; TITLE OF INVENTION: DNA Encoding CAI Resistance Proteins and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/900,321
; FILING DATE: 25-JUL-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,190
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-204100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 5:
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; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-900-321-5

Query Match 44.3%; Score 27; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11  
|||  
Db 1 VPPAPVPC 8

RESULT 5  
PCT-US95-03610-5  
; Sequence 5, Application PC/TUS9503610  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: DNA ENCODING CAI RESISTANCE PROTEINS AND  
; TITLE OF INVENTION: US95 THEROP  
; NUMBER OF SEQUENCES: 10  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US95/03610  
; FILING DATE: 14-MAR-1995  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/212,190  
; FILING DATE: 14-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-204000PC  
; REFERENCE/DOCKET NUMBER: DHHS Ref. No. E-112-94/0  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US95-03610-5

Query Match 44.3%; Score 27; DB 5; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 VPLTSVPC 11  
|||  
Db 1 VPPAPVPC 8

RESULT 6  
US-08-769-745-15  
; Sequence 15, Application US/08769745  
; Patent No. 5955259  
; GENERAL INFORMATION:  
; APPLICANT: Holmes, Todd C.  
; APPLICANT: Levitan, Irwin B.  
; APPLICANT: Brandeis University  
; TITLE OF INVENTION: Mechanism for the Regulation of Ion  
; CHANNEL ACTIVITY

; FILE REFERENCE: BRU96-02  
; CURRENT APPLICATION NUMBER: US/08/769,745  
; CURRENT FILING DATE: 1996-12-19  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 15  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Rat  
US-08-769-745-15

Query Match 42.6%; Score 26; DB 2; Length 6;  
Best Local Similarity 83.3%; Pred. No. 3e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10  
|||  
Db 1 PLTPVP 6

RESULT 7  
US-08-189-331-149  
; Sequence 149, Application US/08189331  
; Patent No. 5747334  
; GENERAL INFORMATION:  
; APPLICANT: Kay, B. K.  
; APPLICANT: Fowlkes, D. M.  
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents  
; NUMBER OF SEQUENCES: 186  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/189,331  
; FILING DATE: Concurrently herewith  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-155  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 149:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-189-331-149

Query Match 42.6%; Score 26; DB 1; Length 8;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 C1SVPLT 7  
|:|:|  
Db 2 CV5APQT 8

RESULT 8  
US-08-471-068-149

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; Sequence 149, Application US/08471068
; Patent No. 5948635
; GENERAL INFORMATION:
; APPLICANT: Kay, B. K.
; APPLICANT: Fowkes, D. M.
; TITLE OF INVENTION: Totally Synthetic Affinity Reagents
; NUMBER OF SEQUENCES: 186
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,068
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/189,331
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-155
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 149:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; PS-08-471-068-149

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Query Match 42.6%; Score 26; DB 2; Length 8;  
Best Local Similarity 57.1%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	1	CISVPLT	7
		:	:
Db	2	CVSAPOT	8

RESULT 9  
US-08-331-383-33  
; Sequence 33, Application US/08331383  
; Patent No. 5605809  
; GENERAL INFORMATION:  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of  
; TITLE OF INVENTION: Processes in Biological Samples and Methods and Use  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible

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, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patent In Release #1.0, Version #1.25
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/08/331.383
, FILING DATE: 28-OCT-1994
, CLASSIFICATION: 424
, ATTORNEY/AGENT INFORMATION:
, NAME: Dow, Karen B.
, REGISTRATION NUMBER: 29,684
, REFERENCE/DOCKET NUMBER: 16865-1
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: 415-326-2400
, TELEFAX: 415-326-2422
, INFORMATION FOR SEQ ID NO: 33:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 9 amino acids
, TYPE: amino acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, US-08-331-383-33
U
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Query Match 41.8%; Score 25.5; DB 1; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy	3	SVPLTSVPC	11
		::: :	
D <sub>b</sub>	2	AIPM-SIPC	9

RESULT 10  
US-08-549-008-43  
; Sequence 43, Application US/08549008  
; Patent No. 5714342  
; GENERAL INFORMATION:  
; APPLICANT: Komoriya, Akira  
; APPLICANT: Packard, Beverly S.  
; TITLE OF INVENTION: Compositions for the Detection of  
; TITLE OF INVENTION: Protease in Biological Samples and Meth  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/549,008  
; FILING DATE: 27-OCT-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/331,383  
; FILING DATE: 28-OCT-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen Lauver  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 016865-000110US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear



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; MOLECULE TYPE: peptide
US-08-549-008-43
Query Match 41.8%; Score 25.5; DB 1; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 11
US-08-802-981-143
; Sequence 143, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-802-981-143
Query Match 41.8%; Score 25.5; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 3e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 3 SVPLTSVPC 11
DB 2 AIPM-SIPC 9

RESULT 12
US-08-360-239B-1
; Sequence 1, Application US/08360239B
; Patent No. 5801222
; GENERAL INFORMATION:
; APPLICANT: Pettit, George R.
; APPLICANT: Tan, Rui
; TITLE OF INVENTION: Isolation and Structure of
; TITLE OF INVENTION: the Human Cancer Cell Growth Inhibitory Cyclic
; TITLE OF INVENTION: Octapeptides Phakellistatin 10 and 11

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Mybeck
; STREET: 8010 East Morgan Trail, #10
; CITY: Scottsdale
; STATE: Arizona
; COUNTRY: USA
; ZIP: 85258-1234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 5
; SOFTWARE: Microsoft Word for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,239B
; FILING DATE: 12/20/94
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard R. Mybeck
; REGISTRATION NUMBER: 17,886
; REFERENCE/DOCKET NUMBER: 4997
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (602)-483-1285
; TELEFAX: (602)-483-7452
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acid residues
; TYPE: amino acid
; TOPOLOGY: Cyclic
; MOLECULE TYPE:
; DESCRIPTION: Cyclooctapeptide
; DESCRIPTION: phakellistatin 10
; HYPOTHETICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: circular
; ORIGINAL SOURCE:
; ORGANISM: Phakellia sp.
; DEVELOPMENTAL STAGE: whole organism
; FEATURE:
; NAME/KEY: Phakellistatin 10
; NAME/KEY: amino acid analysis, high resolution
; NAME/KEY: nuclear magnetic resonance and mass
; NAME/KEY: spectral MS/MS techniques
; OTHER INFORMATION: Phakellistatin 10 is a
; OTHER INFORMATION: cell growth inhibitory peptide with
; OTHER INFORMATION: activity in murine lymphocytic leukemia
; OTHER INFORMATION: cell line of 2.1 mg/ml.
US-08-360-239B-1
Query Match 41.0%; Score 25; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PLTSVP 10
DB 1 PLTPIP 6

RESULT 13
US-08-483-077C-26
; Sequence 26, Application US/08483077C
; Patent No. 5811391
; GENERAL INFORMATION:
; APPLICANT: Arthenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Ellices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics,
; TITLE OF INVENTION: Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
```

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;
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,077C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-CY 1647
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; carboxamide."
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; US-08-483-077C-26
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 44.4%; Pred. No. 3.4e+02;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 ISVPLTSVP 10
; Db 2 LDVPILDVP 10
;
; RESULT 14
; US-08-519-109B-26
; Sequence 26, Application US/08519109B
; Patent No. 5869448
; GENERAL INFORMATION:
; APPLICANT: Arthenius, Thomas S.
; APPLICANT: Tempczyk, Anna
; APPLICANT: Elices, Mariano J.
; APPLICANT: Zheng, Zhong-Li
; TITLE OF INVENTION: Cyclic CS-1 Peptidomimetics.
; TITLE OF INVENTION: Compositions and Methods of Using Same
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,109B
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
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; REFERENCE/DOCKET NUMBER: P-CY 1795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 10
; OTHER INFORMATION: /note= "The carboxy-terminus is a
; carboxamide."
;
; US-08-519-109B-26
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 44.4%; Pred. No. 3.4e+02;
; Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
;
; QY 2 ISVPLTSVP 10
; Db 2 LDVPILDVP 10
;
; RESULT 15
; US-08-482-228-108
; Sequence 108, Application US/08482228
; Patent No. 5968753
; GENERAL INFORMATION:
; APPLICANT: Tseng-Law, Janet
; APPLICANT: Kobori, Joan A.
; APPLICANT: Al-Abdaly, Fahad A.
; APPLICANT: Guillermo, Roy
; APPLICANT: Helgeson, Sam L.
; APPLICANT: Deans, Robert J.
; TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
; TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
; NUMBER OF SEQUENCES: 215
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janice Guthrie, Ph.D.
; STREET: P.O. Box 15210
; CITY: Irvine
; STATE: California
; COUNTRY: USA
; ZIP: 92713-5210
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,228
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Guthrie, Janice
; REGISTRATION NUMBER: 35,170
; REFERENCE/DOCKET NUMBER: IT-4630CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 440-5353
; TELEFAX: (714) 553-1952
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
;
; US-08-482-228-108
;
; Query Match 41.0%; Score 25; DB 2; Length 10;
; Best Local Similarity 66.7%; Pred. No. 3.4e+02;
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Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CTSVPLTSV 9  
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Db 2 CIDVFLTCV 10

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Job time : 21 secs

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**This Page Blank (uspto)**

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:52:56 ; Search time 21 Seconds  
(without alignments)  
77.869 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCRPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2990

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	34	34.0	16	2 PH1477	T-cell receptor be
2	33.5	33.5	12	2 PT0216	T-cell receptor be
3	32	32.0	16	2 PH1472	T-cell receptor be
4	32	32.0	16	2 PH1473	T-cell receptor be
5	32	32.0	16	2 PH1480	T-cell receptor be
6	30	30.0	12	2 S47394	T-cell antigen rec
7	29.5	29.5	13	2 S47357	T-cell antigen rec
8	29	29.0	12	2 S26549	T-cell receptor be
9	29	29.0	14	2 G44957	photosystem II oxy
10	29	29.0	17	2 C24166	photosystem II ext
11	28	28.0	12	2 PH1463	T-cell receptor be
12	28	28.0	12	2 PH1466	T-cell receptor be
13	28	28.0	13	2 S47400	T-cell antigen rec
14	28	28.0	16	2 PH1474	T-cell antigen rec
15	27	27.0	11	2 PT0217	T-cell receptor be
16	27	27.0	12	2 S47391	T-cell receptor be
17	27	27.0	13	2 S47383	T-cell antigen rec
18	27	27.0	14	2 PA0013	photosystem II oxy
19	27	27.0	16	2 PH1476	T-cell receptor be
20	27	27.0	17	2 S57519	T-cell receptor V-
21	26	26.0	11	2 S57575	T-cell antigen rec
22	26	26.0	12	2 S47395	T-cell receptor be
23	26	26.0	13	2 S47381	T-cell antigen rec
24	26	26.0	15	2 B49655	T-cell receptor be
25	25.5	25.5	13	2 S47382	T-cell antigen rec
26	25.5	25.5	15	2 PH0752	T-cell receptor be
27	25.5	25.5	15	2 PH0760	T-cell receptor be
28	25	25.0	10	2 S23371	T-cell receptor al
29	25	25.0	11	2 PH0947	T-cell receptor be

30	25	25.0	12	2 PH1469	T-cell receptor be
31	25	25.0	12	2 PH0931	T-cell receptor be
32	25	25.0	14	2 PH0753	T-cell receptor be
33	25	25.0	15	2 PH0808	T-cell receptor al
34	25	25.0	17	2 C49255	T-cell receptor be
35	24.5	24.5	12	2 PH1457	T-cell receptor be
36	24	24.0	11	2 PH1583	Ig H chain V-D-J r
37	24	24.0	12	2 S26552	T-cell receptor be
38	24	24.0	12	2 S26559	T-cell receptor be
39	24	24.0	12	2 S26554	T-cell receptor be
40	24	24.0	12	2 S47363	T-cell receptor be
41	24	24.0	12	2 PH1467	T-cell antigen rec
42	24	24.0	12	2 PH1468	T-cell receptor be
43	24	24.0	13	2 A28953	alpha-conotoxin SI
44	24	24.0	13	2 S47390	T-cell antigen rec
45	24	24.0	15	1 NTKNAG	alpha-conotoxin GI

#### ALIGNMENTS

##### RESULT 1

PH1477

T-cell receptor beta chain (clone A3/H2R5) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995

R:Accession: PH1477

R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko J. Exp. Med. 177, 811-820, 1993

A>Title: T cell receptor selection by and recognition of two class I major histocompatib

A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1477

A:Molecule type: mRNA

A:Residues: 1-16 <CAS>

A:Experimental source: cytolytic T-lymphocyte

C:Superfamily: immunoglobulin homology

C:Keywords: receptor; T-cell

Query Match 34.0%; Score 34; DB 2; Length 16;

Best Local Similarity 60.0%; Pred. No. 70;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CASELGKSTN 10

Db 1 CASSVGTGTN 10

##### RESULT 2

PT0216

T-cell receptor beta chain V-J region (4-1-G.4) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997

C:Accession: PT0216

R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A>Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric

A:Reference number: PT0209; MUID:91217621; PMID:1902501

A:Accession: PT0216

A:Molecule type: mRNA

A:Residues: 1-12 <NAK>

C:Keywords: T-cell receptor

Query Match 33.5%; Score 33.5; DB 2; Length 12;

Best Local Similarity 72.7%; Pred. No. 65;

Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 CASELGKSTNT 11

Db 1 CASSLG-TTNT 10

##### RESULT 3

PH1472

T-cell receptor beta chain (clone A24/12.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1472  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1472  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTN 10  
||| |||  
DB 1 CASSLGTGNN 10

## RESULT 4

PH1473  
T-cell receptor beta chain (clone A3/IIIC5) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1473  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911  
A:Accession: PH1473  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;  
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTN 10  
||| |||  
DB 1 CASSYGTGIN 10

## RESULT 5

PH1480  
T-cell receptor beta chain - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 27-Oct-1995  
C:Accession: PH1480; PH1478  
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:8436911

A:Accession: PH1480  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS1>  
A:Experimental source: cytolytic T-lymphocyte, clone A3/C80b  
A:Accession: PH1478  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS2>  
A:Experimental source: cytolytic T-lymphocyte, clone A24/PEF5  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 32.0%; Score 32; DB 2; Length 16;  
Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CASELGKSTN 10  
||| |||  
DB 1 CASSGTGTGN 10

## RESULT 6

S47394  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47394; S47369  
R;Lehner, P.J.  
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A:Reference number: S47355  
A:Accession: S47394  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-12 <LEH>  
A:Cross-references: EMBL:Z35714; NID:G527523; PIDN:CAA84783.1; PID:G527524; EMBL:Z35694;  
C:Keywords: T-cell receptor

Query Match 30.0%; Score 30; DB 2; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTF 12  
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DB 1 CASSIGNGYTF 12

## RESULT 7

S47357  
T-cell antigen receptor VJ junction beta chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C:Accession: S47357  
R;Lehner, P.J.  
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T  
A:Reference number: S47355  
A:Accession: S47357  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-13 <LEH>  
A:Cross-references: EMBL:Z35691; NID:G527451; PIDN:CAA84750.1; PID:G527452  
C:Keywords: T-cell receptor

Query Match 29.5%; Score 29.5; DB 2; Length 13;  
Best Local Similarity 63.6%; Pred. No. 2.9e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 CASELGKSTNT 11  
||| : |||  
DB 1 CASS-GRSTDT 10

## RESULT 8

S26549  
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 13-Jan-1995 #sequence\_revision 17-Apr-1998 #text\_change 17-Mar-1999  
C:Accession: S26549; S26550  
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi  
J. Exp. Med. 176, 439-447, 1992  
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto  
A:Reference number: S26512; MUID:92364546; PMID:1380061  
A:Accession: S26549  
A:Molecule type: mRNA  
A:Residues: 1-12 <CAS>  
A:Cross-references: EMBL:X67999

A;Experimental source: cytolytic T-lymphocyte, clone Cw3/A8  
 A;Accession: S26550  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CA2>  
 A;Cross-references: EMBL:X68000  
 A;Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: T-cell receptor

Query Match 29.0%; Score 29; DB 2; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 3.3e+02;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGKS 8  
 ||| |||:  
 Db 1 CASSLGET 8

RESULT 9  
 G44957  
 photosystem II oxygen-evolving complex protein 2 - common tobacco (cv. Samsun NN) (fragm  
 C;Species: Nicotiana tabacum (common tobacco)  
 C;Date: 03-Jun-1993 #sequence\_revision 03-Jun-1993 #text\_change 18-Jun-1993  
 C;Accession: G44957  
 R;Akeda, S.; Sato, F.; Ida, K.; Yamada, Y.  
 Plant Cell Physiol. 31, 215-221, 1990  
 A;Title: Characterization of polypeptides that accumulate in cultured Nicotiana tabacum  
 A;Reference number: A44957  
 A;Accession: G44957  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-14 <TAK>

Query Match 29.0%; Score 29; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3.7e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GKSTNTFCCK 15  
 ||: ||| |||  
 Db 3 GEANVFGKP 12

RESULT 10  
 C24166  
 photosystem II extrinsic membrane protein - spinach (fragment)  
 C;Species: Spinacia oleracea (spinach)  
 C;Date: 05-Jun-1987 #sequence\_revision 21-May-1988 #text\_change 24-Apr-1998  
 C;Accession: C24166  
 R;Water, J.; Sainikow, J.; Jansson, C.  
 FEBS Lett. 203, 230-234, 1986  
 A;Title: N-terminal sequence determination and secondary structure analysis of extrinsic  
 A;Reference number: A24166  
 A;Accession: C24166  
 A;Molecule type: protein  
 A;Residues: 1-17 <VAI>  
 C;Superfamily: photosystem II oxygen-evolving complex protein 2  
 C;Keywords: chloroplast; membrane protein; thylakoid

Query Match 29.0%; Score 29; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 GKSTNTFCCK 15  
 ||: ||| |||  
 Db 2 GEANVFGKP 11

RESULT 11  
 PH1463  
 T-cell receptor beta chain (clone A24/10.1) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C;Accession: PH1463

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
 J. Exp. Med. 177, 811-820, 1993  
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
 A;Reference number: PH1430; MUID:93171821; PMID:8436911  
 A;Accession: PH1463  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>  
 A;Experimental source: cytolytic T-lymphocyte  
 C;Superfamily: immunoglobulin homology  
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;  
 Best Local Similarity 62.5%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CASELGKS 8  
 ||| |||:  
 Db 1 CASSLGNT 8

RESULT 12  
 PH1466  
 T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C;Accession: PH1466  
 R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko  
 J. Exp. Med. 177, 811-820, 1993  
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
 A;Reference number: PH1430; MUID:93171821; PMID:8436911  
 A;Accession: PH1466  
 A;Molecule type: mRNA  
 A;Residues: 1-12 <CAS>  
 A;Experimental source: cytolytic T-lymphocyte  
 C;Superfamily: immunoglobulin homology  
 C;Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 12;  
 Best Local Similarity 71.4%; Pred. No. 4.7e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CASELGK 7  
 ||| |||:  
 Db 1 CASSLGQ 7

RESULT 13  
 S47400  
 T-cell antigen receptor VJ junction beta chain - human  
 C;Species: Homo sapiens (man)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999  
 C;Accession: S47400  
 R;Löhner, P.J.  
 submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c  
 A;Reference number: S47355  
 A;Accession: S47400  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-13 <LEH>  
 A;Cross-references: EMBL:Z35678; NID:g527535; PIDN:CAA84747.1; PID:g527536  
 C;Keywords: T-cell receptor

Query Match 28.0%; Score 28; DB 2; Length 13;  
 Best Local Similarity 41.7%; Pred. No. 5e+02;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CASELGKSTNTP 12  
 ||| |||:  
 Db 1 CASSVALATEAF 12

RESULT 14

PH1474  
T-cell receptor beta chain (clone A2/25) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
C:Accession: PH1474  
J.Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K  
J. Exp. Med. 177, 811-820, 1993  
A:Title: T cell receptor selection by and recognition of two class I major histocompatib  
A:Reference number: PH1430; MUID:93171821; PMID:9436911  
A:Accession: PH1474  
A:Molecule type: mRNA  
A:Residues: 1-16 <CAS>  
A:Experimental source: cytolytic T-lymphocyte  
C:Superfamily: immunoglobulin homology  
C:Keywords: receptor; T-cell

Query Match 28.0%; Score 28; DB 2; Length 16;  
Best Local Similarity 50.0%; Pred. No. 6e+02;  
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
  
QY 1 CASELGKSTN 10  
||| |  
Db 1 CASSFGTGNN 10

RESULT 15  
PT0217  
T-cell receptor beta chain V-J region (4-1-E.2) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 30-May-1997  
C:Accession: PT0217  
R.Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.  
J. Exp. Med. 173, 1091-1097, 1991  
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric  
A:Reference number: PT0209; MUID:91217621; PMID:1902501  
A:Accession: PT0217  
A:Molecule type: mRNA  
A:Residues: 1-11 <NAK>  
C:Keywords: T-cell receptor

Query Match 27.0%; Score 27; DB 2; Length 11;  
Best Local Similarity 83.3%; Pred. No. 6.2e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 CASELG 6  
||| |  
Db 1 CASRLG 6

Search completed: September 5, 2004, 10:56:30  
Job time : 21 secs



Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	27	27.0	14	1	CX1A_CONBE	P58623 conus betul
2	26	26.0	12	1	PGP3_PHYPA	P80662 physcomitre
3	25.5	25.5	15	1	UC19_MA1ZE	P80625 zea mays (m
4	24	24.0	15	1	CXA1_CONGE	P01519 conus geogr
5	23	23.0	13	1	CXA2_CONGE	P01520 conus geogr
6	23	23.0	13	1	CXAA_CONST	P28878 conus stria
7	23	23.0	13	1	PSBP_PINPS	P81668 pinus pinas
8	23	23.0	14	1	CXA1_CONGN	P56973 conus conso
9	23	23.0	14	1	CXA1_CONMA	P01521 conus magus
10	23	23.0	15	1	CX1B_CONBE	P58624 conus betul
11	23	23.0	15	1	CXA2_CONAL	P56640 conus aulic
12	23	23.0	16	1	CXA3_CONAL	P56639 conus aulic
13	23	23.0	16	1	CXA3_CONAL	P56641 conus aulic
14	23	23.0	16	1	CXAA_CONPE	P50984 conus penna
15	23	23.0	16	1	CXAB_CONPE	P50985 conus penna
16	22	22.0	15	1	AFCA_STRP5	P58827 streptococc
17	22	22.0	15	1	NXSO_PSETE	P59073 pseudonaja
18	21	21.0	12	1	CXL3_CONMR	P58809 conus marmo
19	21	21.0	12	1	CXST_CONTE	P58846 conus texti
20	21	21.0	15	1	SODM_STRGR	P80733 streptomyce
21	20	20.0	12	1	UR2B_CATCO	P04559 catostomus
22	20	20.0	12	1	V23K_WSSV	P82005 white spot
23	20	20.0	13	1	LIGA_TRAVE	P20011 trametes ve
24	20	20.0	14	1	JAP1_RANJA	P83305 tana japoni
25	19	19.0	7	1	TPFY_PACDA	P83455 pachymedusa
26	19	19.0	7	1	UF04_MOUSE	P38642 mus musculu
27	19	19.0	10	1	C0XM_RAT	P80431 rattus norv
28	19	19.0	11	1	CX5A_CONAL	P58848 conus aulic
29	19	19.0	11	1	CX5B_CONAL	P58849 conus aulic
30	19	19.0	12	1	FAR7_PENNO	P83322 penaeus mon
31	19	19.0	13	1	FARB_ASCSU	P43173 ascaris suu
32	19	19.0	15	1	CX3A_CONQU	P58841 conus querc
33	19	19.0	15	1	CX3B_CONQU	P58842 conus querc

RA Kasten B., Buck F., Nuske J., Reski R.;  
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting  
RL plastid enzymes.";  
RL Planta 201:261-272(1997).  
CC -!- FUNCTION: May be involved in the regulation of photosystem II.  
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated  
CC with the photosystem II complex.  
CC -!- INDUCTION: By light.  
CC -!- SIMILARITY: Belongs to the psbp family.  
CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;  
KW Multigene family.  
FT NON\_TER 12 12  
SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C44DC5 CRC64;  
Query Match 26.0%; Score 26; DB 1; Length 12;  
Best Local Similarity 50.0%; Pred. No. 2.3e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 6 GKSTWTFCKP 15  
|:|:|:|:  
Db 3 GRSANVFQAP 12  
|:|:|:|:  
RESULT 3  
UC19 MAIZE STANDARD; PRT; 15 AA.  
ID UC19 MAIZE  
AC P80625;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernicelli J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program.";  
RL Theor. Appl. Genet. 93:997-1005(1996).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 5.6, its MW is: 18.4 kDa.  
DR Maize-2DPAGE; P80625; COLEOPTILE.  
DR MaizeDB; 123951; -. 1  
FT NON\_TER 1 1  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;  
Query Match 25.5%; Score 25.5; DB 1; Length 15;  
Best Local Similarity 41.7%; Pred. No. 3.5e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;  
QY 6 GKSTWTFCKP 16  
|:|:|:|:  
Db 2 GRRVTTGCSPP 13  
|:|:|:|:  
RESULT 4  
CXAL CONGE STANDARD; PRT; 15 AA.  
ID CXAL CONGE  
AC P01579;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Alpha-conotoxin GIA [contains: Alpha-conotoxin GI (GI)].  
OS Conus geographus (Geography cone).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
OC

OC Neogastropoda; Conoidea; Conidae; Conus.  
OX NCBI\_TaxID=6491;  
RN [1]  
RP SEQUENCE.  
RA MEDLINE=81191854; PubMed=7014556;  
RA Gray W.R., Luque F.A., Olivera B.M., Barrett J., Cruz L.J.;  
RT "Peptide toxins from Conus geographus venom.";  
RL J. Biol. Chem. 256:4734-4740(1981).  
RN [2]  
RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.  
RX MEDLINE=83105694; PubMed=7152021;  
RA Nishiuchi Y., Sakakibara S.;  
RT "Primary and secondary structure of conotoxin GI, a neurotoxic  
RT tridecapeptide from a marine snail.";  
RL FEBS Lett. 148:260-262(1982).  
RN [3]  
RP DISULFIDE BONDS OF GI, AND SYNTHESIS OF GI.  
RX MEDLINE=84280842; PubMed=6466616;  
RA Gray W.R., Luque F.A., Galyean R., Atherton E., Sheppard R.C.,  
RA Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,  
RA Cruz L.J., Rivier J.;  
RT "Conotoxin GI: disulfide bridges, synthesis, and preparation of  
RT iodinated derivatives.";  
RL Biochemistry 23:2796-2802(1984).  
RN [4]  
RP COMPARISON WITH ALPHA-CONOTOXIN SI AND ALPHA-CONOTOXIN MI.  
RX MEDLINE=95034849; PubMed=7947815;  
RA Hann R.M., Pagan O.R., Sterovic V.A.;  
RT "The alpha-conotoxins GI and MI distinguish between the nicotinic  
RT acetylcholine receptor agonist sites while SI does not.";  
RL Biochemistry 33:14058-14063(1994).  
RN [5]  
RP PHARMACOLOGICAL CHARACTERIZATION ON MOUSE MUSCLE-DERIVED BC3H-1 CELLS  
RP AND TORPEDO ELECTRIC ORGAN.  
RX MEDLINE=95349531; PubMed=7623764;  
RA Groebe D.R., Dumm J.M., Levitan E.S., Abramson S.N.;  
RT "alpha-Conotoxins selectively inhibit one of the two acetylcholine  
RT binding sites of nicotinic receptors.";  
RL Mol. Pharmacol. 48:105-111(1995).  
RN [6]  
RP MUTAGENESIS OF ARG-9.  
RX MEDLINE=97317090; PubMed=9174364;  
RA Groebe D.R., Gray W.R., Abramson S.N.;  
RT "Determinants involved in the affinity of alpha-conotoxins GI and SI  
RT for the muscle subtype of nicotinic acetylcholine receptors.";  
RL Biochemistry 36:6469-6474(1997).  
RN [7]  
RP X-RAY CRYSTALLOGRAPHY (1.2 ANGSTROMS) OF GI.  
RX MEDLINE=96378624; PubMed=8784187;  
RA Guddat L.W., Martin J.A., Shan L., Edmundson A.B., Gray W.R.;  
RT "Three-dimensional structure of the alpha-conotoxin GI at 1.2-A  
RT resolution.";  
RL Biochemistry 35:11329-11335(1996).  
RN [8]  
RP STRUCTURE BY NMR OF GI.  
RX MEDLINE=89352562; PubMed=2765514;  
RA Kobayashi Y., Ohkubo T., Kyogoku Y., Nishiuchi Y., Sakakibara S.,  
RA Braun W., Go N.;  
RT "Solution conformation of conotoxin GI determined by 1H nuclear  
RT magnetic resonance spectroscopy and distance geometry calculations.";  
RL Biochemistry 28:4853-4860(1989).  
RN [9]  
RP STRUCTURE BY NMR OF GI.  
RX MEDLINE=89375269; PubMed=2775719;  
RA Pardi A., Galdes A., Florance J., Maniconte D.;  
RT "Solution structures of alpha-conotoxin GI determined by two-  
RT dimensional NMR spectroscopy.";  
RL Biochemistry 28:5494-5501(1989).  
RN [10]  
RP STRUCTURE BY NMR OF GI.  
RX MEDLINE=98321613; PubMed=9660176;  
RA Maslennikov I.V., Sobol A.G., Gladky K.V., Lugovskoy A.A.,  
RA Ostrovsky A.G., Tsetlin V.I., Ivanov V.T., Arseniev A.S.;

OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.
OK	NCBI_TaxID=6491;
OK	[1]
RN	SEQUENCE.
RP	
RX	MEDLINE=61191854; PubMed=7014556;
RA	Gray W.R., Lucue A., Olivera B.M., Barrett J., Cruz L.J.;
RA	"Peptide toxins from Conus geographus venom.;"
RT	J. Biol. Chem. 256:4734-4740(1981).
RL	[2]
RN	DISULFIDE BONDS.
RP	MEDLINE=84280842; PubMed=6466616;
RX	Gray W.R., Lucue F.A., Galyean R., Atherton E., Sheppard R.C.,
RA	Stone B.L., Reyes A., Alford J., McIntosh M., Olivera B.M.,
RA	Cruz L.J., Rivier J.;
RA	"Conotoxin GI: disulfide bridges, synthesis, and preparation of
RT	iodinated derivatives.;"
RL	Biochemistry 23:2796-2802(1984).
CC	-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC	bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC	inhibit them.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC	family.
DR	PIR; A01783; NTKN2G.
DR	HSP; P56973; 1845.
KW	Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW	Acetylcholine receptor inhibitor; Amidation.
FT	DISULFID 2 7
FT	DISULFID 3 13
FT	MOD RES 13 13
FT	SEQUENCE 13 AA; 1422 MW; DDEE831C39297BED CRC64;
QY	Query Match 23.0%; Score 23; DB 1; Length 13;
DB	Best Local Similarity 60.0%; Pred. No. 7.9e+02;
	Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	13 CKPPC 17
	3 CHPAC 7
RESULT 6	
IC	CXAA CONST
ID	CXAA CONST STANDARD; PRT; 13 AA.
AC	P28878;
DT	01-DEC-1992 (Rel. 24, Created)
DT	01-DEC-1992 (Rel. 24, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Alpha-conotoxin SIA (SIA).
OS	Conus striatus (Striated cone).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC	Neogastropoda; Conoidea; Conidae; Conus.
OK	NCBI_TaxID=6493;
RN	[1]
RP	SEQUENCE.
RX	TISSUE=Venom;
RA	MEDLINE=91369955; PubMed=1892838;
RA	Myers R.A., Zafarella G.C., Gray W.R., Abbot J., Cruz L.J.,
RA	Olivera B.M.;
RA	"Alpha-conotoxins, small peptide probes of nicotinic acetylcholine
RT	receptors.;"
RL	Biochemistry 30:9370-9377(1991).
CC	-!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC	bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC	inhibit them.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC	family.
DR	PIR; A40312; NTKVAS

KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 7  
 FT DISULFID 3 13  
 FT MOD\_RES 13 13  
 SQ SEQUENCE 13 AA; 1461 MW; DEF1931982457BBD CRC64;  
 AMIDATION.  
 Query Match 23.0%; Score 23; DB 1; Length 13;  
 Best Local Similarity 60.0%; Pred. No. 7.9e+02;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 13 CKPPC 17  
 Db 3 CHPAC 7  
 RESULT 7  
 PSBP PINPS STANDARD; PRT; 13 AA.  
 AC P81668;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Oxygen-evolving enhancer protein 2 (ORE2) (23 kDa subunit of oxygen  
 DE evolving system of photosystem II) (Fragment).  
 GN PSBP.  
 OS Pinus pinaster (Maritime pine).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.  
 OX NCBI\_TaxID=71647;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Needle;  
 RX MEDLINE=99274088; PubMed=10344291;  
 RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,  
 RA Frigerio J.-M., Plomion C.;  
 RT "Separation and characterization of needle and xylem maritime pine  
 RT proteins.";  
 RL Electrophoresis 20:1098-1108(1999).  
 CC -!- FUNCTION: May be involved in the regulation of photosystem II.  
 CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated  
 CC with the photosystem II complex (By similarity).  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this protein  
 CC (spot N179) is: 5.9, its MW is: 22 kDa.  
 CC -!- SIMILARITY: Belongs to the psbp family.  
 CC Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane.  
 KW NON\_TER 13 13  
 FT SEQUENCE 13 AA; 1294 MW; C6772B0D54D7C44D CRC64;  
 SQ  
 Query Match 23.0%; Score 23; DB 1; Length 13;  
 Best Local Similarity 40.0%; Pred. No. 7.9e+02;  
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 QY 6 GKSTNTFCPK 15  
 Db 3 GEANVFGAP 12  
 RESULT 8  
 CXAL CONCN STANDARD; PRT; 14 AA.  
 AC P56973;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin CN1A [Contains: Alpha-conotoxin CN1B].  
 OS Conus consors (Singed cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=101297;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, CHARACTERIZATION, AND STRUCTURE BY NMR.

RC TISSUE=Venom;  
 RX MEDLINE=99255390; PubMed=10320362;  
 RA Favreau P., Krimm I., le Gall F., Bobenrieth M.J., Lamthanh H.,  
 RA Bouet P., Servent D., Molgo J., Menez A., Letourneux Y.,  
 RA Lancelin J.-M.;  
 RT "Biochemical characterization and nuclear magnetic resonance  
 RT structure of novel alpha-conotoxins isolated from the venom of Conus  
 RT consors.";  
 RL Biochemistry 38:6317-6326(1999).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide seems to be a potent and selective  
 CC blocker of muscular subtype of nAChR.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A58963; A58963.  
 DR PDB; 1B45; 09-JUL-99.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 FT PEPTIDE 1 14 ALPHA-CONOTOXIN CN1A.  
 FT PEPTIDE 3 14 ALPHA-CONOTOXIN CN1B.  
 FT DISULFID 3 8  
 FT DISULFID 4 14  
 FT MOD\_RES 14 14  
 FT HELIX 6 8  
 FT TURN 9 10  
 SQ SEQUENCE 14 AA; 1548 MW; DEEE91969BPF5E5BD CRC64;  
 Query Match 23.0%; Score 23; DB 1; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 13 CKPPC 17  
 Db 4 CHPAC 8  
 RESULT 9  
 CXAL CONCN STANDARD; PRT; 14 AA.  
 ID CXAL CONCN  
 AC P01521;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin MI (M1).  
 OS Conus magus (Magus cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=6492;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=83073458; PubMed=7149738;  
 RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;  
 RT "Isolation and structure of a peptide toxin from the marine snail  
 RT Conus magus.";  
 RL Arch. Biochem. Biophys. 218:329-334(1982).  
 RN [2]  
 RP DISULFIDE BONDS.  
 RX MEDLINE=84032400; PubMed=6630187;  
 RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;  
 RT "Conotoxin MI. Disulfide bonding and conformational states.";  
 RL J. Biol. Chem. 258:12247-12251(1983).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A01784; NTKN1M.

DR HSP: P56973; 1B45.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 3 8  
 FT DISULFID 4 14  
 FT MOD RES 14 14  
 SQ SEQUENCE 14 AA; 1499 MW; DEEE1898BF5E5BD CRC64;  
 Query Match 23.0%; Score 23; DB 1; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 8.5e+02;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 13 CKPCC 17  
 Db 4 CHPAC 8  
 RESULT 10  
 CX1B CONBE STANDARD; PRT; 15 AA.  
 AC P5624;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Conotoxin BetXib.  
 OS Conus betulinus (Beech cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89764;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20058566; PubMed=10591037;  
 RA Chen J.-S., Fan C.-X., Hu K.-P., Wei K.-H., Zhong M.-N.;  
 RT "Studies on conotoxins of Conus betulinus";  
 RL J. Nat. Toxins 8:341-349(1999).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1642.5; METHOD=MALDI.  
 CC -!- SIMILARITY: BELONGS TO THE M-SUPERFAMILY OF CONOTOXINS.  
 KW Neurotoxin; Toxin.  
 FT DISULFID 1 9  
 FT DISULFID 2 12  
 FT DISULFID 6 13  
 SQ SEQUENCE 15 AA; 1650 MW; 3749B4F08E311337 CRC64;  
 Query Match 23.0%; Score 23; DB 1; Length 15;  
 Best Local Similarity 60.0%; Pred. No. 9.1e+02;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 13 CKPCC 17  
 Db 2 CELPC 6  
 RESULT 11  
 CXA2 CONAL STANDARD; PRT; 15 AA.  
 AC P5640;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-conotoxin AulB.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RT "Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic  
 acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Olivera B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic  
 acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 RN [2]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=20187585; PubMed=10722709;  
 RA Cho J.H., Mok K.H., Olivera B.M., McIntosh J.M., Park K.H., Han K.H.;  
 RT "Nuclear magnetic resonance solution conformation of alpha-conotoxin  
 AulB, an alpha(3)beta(4) subtype-selective neuronal nicotinic  
 acetylcholine receptor antagonist";  
 RL J. Biol. Chem. 275:8680-8685(2000).  
 RN [3]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=22359066; PubMed=12376538;  
 RA Dutton J.L., Bansal P.S., Hogg R.C., Adams D.J., Alewood P.F.,  
 RA Craik D.J.;  
 RT "A new level of conotoxin diversity, a non-native disulfide bond  
 connectivity in alpha-conotoxin AulB reduces structural definition  
 but increases biological activity.";  
 RL J. Biol. Chem. 277:48849-48857(2002).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -!- MASS SPECTROMETRY: MW=1572.5; METHOD=Electrospray.  
 CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PDB; 1DG2; 23-MAY-00.  
 DR PDB; 1MXN; 30-DEC-02.  
 DR PDB; 1NXP; 30-DEC-02.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; 3D-structure.  
 FT DISULFID 2 8  
 FT DISULFID 3 15  
 FT MOD RES 15 15  
 SQ SEQUENCE 15 AA; 1578 MW; 84EFE95FDC700155 CRC64;  
 Query Match 23.0%; Score 23; DB 1; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 15 PPC 17  
 Db 6 PPC 8  
 RESULT 12  
 CXA1 CONAL STANDARD; PRT; 16 AA.  
 AC P56639;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Alpha-conotoxin AulA.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RT "Alpha-conotoxin AulB selectively blocks alpha3 beta4 nicotinic  
 acetylcholine receptors and nicotine-evoked norepinephrine release.";  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they

CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=1725.6; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A59045; A59045.  
 DR HSPSP; P50984; 1PEN.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT MOD\_RES 3 16  
 FT SEQUENCE 16 AA; 1731 MW; 1E310FB8FDC7001 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;  
 QY 15 PPC 17  
 DB 6 PPC 8

RESULT 13  
 CXA3\_CONAL STANDARD; PRT; 16 AA.  
 ID \_CXA3\_CONAL STANDARD; PRT; 16 AA.  
 AC P56641;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin AuIC.  
 OS Conus aulicus (Court cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 ON NCBI\_TaxID=89437;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=99003392; PubMed=9786965;  
 RA Luo S., Kulak J.M., Cartier G.E., Jacobsen R.B., Yoshikami D.,  
 RA Olivera B.M., McIntosh J.M.;  
 RT "Alpha-conotoxin AuIB selectively blocks alpha3 beta4 nicotinic  
 RT acetylcholine receptors and nicotine-evoked norepinephrine release."  
 RL J. Neurosci. 18:8571-8579(1998).  
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. This peptide blocks mammalian nicotinic  
 CC acetylcholine receptors composed of alpha-3/beta-4 subunits.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- MASS SPECTROMETRY: MW=1667.6; METHOD=Electrospray.  
 CC -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; C59045; C59045.  
 DR HSPSP; P50984; 1PEN.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation.  
 FT DISULFID 2 8  
 FT MOD\_RES 3 16  
 FT SEQUENCE 16 AA; 1673 MW; 1E310D3B8FDC7001 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;  
 QY 15 PPC 17  
 DB 6 PPC 8

RESULT 14  
 CXAA\_CONPE STANDARD; PRT; 16 AA.  
 ID \_CXAA\_CONPE STANDARD; PRT; 16 AA.  
 AC P50984;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Alpha-conotoxin PnIA.  
 OS Conus pennaceus (Feathered cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 ON NCBI\_TaxID=37335;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Venom;  
 RX MEDLINE=94347719; PubMed=8068627;  
 RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,  
 RA Fainzilber M., Zlotkin E.;  
 RA Spira M.E., Zlotkin E.;  
 RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal  
 RT acetylcholine receptors";  
 RT Biochemistry 33:9523-9529(1994).  
 RN [2]  
 RP SULFATION OF TYR-15.  
 RX MEDLINE=99242956; PubMed=10226369;  
 RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,  
 RA Baldwin M.A., Burlingame A.L.;  
 RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins  
 RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and  
 RT phosphopeptides by electrospray, matrix-assisted laser  
 RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass  
 RT spectrometry";  
 RL J. Mass Spectrom. 34:447-454(1999).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).  
 RX MEDLINE=96311277; PubMed=8740364;  
 RA Hu S.-H., Gehrman J., Guddat L.W., Alewood P.F., Craik D.J.,  
 RA Martin J.L.;  
 RT "The 1.1 A crystal structure of the neuronal acetylcholine receptor  
 RT antagonist, alpha-conotoxin PnIA from Conus pennaceus";  
 RL Structure 4:417-423(1996).  
 CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they  
 CC bind to the nicotinic acetylcholine receptors (nAChR) and thus  
 CC inhibit them. In contrast to other alpha-conotoxins, which are  
 CC selective for vertebrate skeletal muscle nAChR, the Conus  
 CC pennaceus alpha-conotoxins block nAChR in mollusks.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -1- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type  
 CC family.  
 DR PIR; A54877; A54877.  
 DR PDB; 1PEN; 21-APR-97.  
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;  
 KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.  
 FT DISULFID 2 8  
 FT MOD\_RES 3 16  
 FT MOD\_RES 15 15  
 FT MOD\_RES 16 16  
 FT HELIX 2 4  
 FT HELIX 6 11  
 FT TURN 13 16  
 FT SEQUENCE 16 AA; 1628 MW; 05310FF95EC99005 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.7e+02; Indels 0;  
 Matches 3; Conservative 0; Mismatches 0; Gaps 0;  
 QY 15 PPC 17  
 DB 6 PPC 8

Job time : 15 secs

RESULT 15

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CXAB CONPE
ID CXAB CONPE STANDARD; PRT; 16 AA.
AC P50985;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alpha-conotoxin PnIB.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94347719; PubMed=8068627;
RA Fainzilber M., Hasson A., Oren R., Burlingame A.L., Gordon D.,
RA Spira M.E., Zlotkin E.;
RT "New mollusc-specific alpha-conotoxins block Aplysia neuronal
RT acetylcholine receptors.";
RL Biochemistry 33:9523-9529(1994).
RN [2]
RP SULFATION OF TYR-15.
RX MEDLINE=99242956; PubMed=10226369;
RA Wolfender J.L., Chu F., Ball H., Wolfender F., Fainzilber M.,
RA Baldwin M.A., Burlingame A.L.;
RT "Identification of tyrosine sulfation in Conus pennaceus conotoxins
RT alpha-PnIA and alpha-PnIB: further investigation of labile sulfo- and
RT phosphopeptides by electrospray, matrix-assisted laser
RT desorption/ionization (MALDI) and atmospheric pressure MALDI mass
RT spectrometry.";
RL J. Mass Spectrom. 34:447-454(1999).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
RX MEDLINE=97444322; PubMed=9298951;
RA Hu S.H., Gehrmann J., Alewood P.F., Craik D.J., Martin J.L.;
RT "Crystal structure at 1.1-A resolution of alpha-conotoxin PnIB:
RT comparison with alpha-conotoxins PnIA and GI.";
RL Biochemistry 36:11323-11330(1997).
CC -!- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. In contrast to other alpha-conotoxins, which are
CC selective for vertebrate skeletal muscle nAChR, the Conus
CC pennaceus alpha-conotoxins block nAChR in mollusks.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the conotoxin A-superfamily. Alpha-type
CC family.
DR PIR; B54877.
DR PDB; 1AKG; 20-MAY-98.
KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
KW Acetylcholine receptor inhibitor; Amidation; Sulfation; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 16
FT MOD_RES 15 15 SULFATION.
FT MOD_RES 16 16 AMIDATION.
FT HELIX 2 4
FT HELIX 6 11
FT TURN 13 16
SQ SEQUENCE 16 AA; 1643 MW; 05310FF95ED86AF5 CRC64;

Query Match 23.0%; Score 23; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PPC 17
Db 6 PPC 8

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Search completed: September 5, 2004, 10:54:59

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:51:46 ; Search time 57 Seconds  
(without alignments)  
94.102 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCCKPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 5061

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.0	13	13	O8QZ5 fugu rubrip
2	26	26.0	13	12	Q918t4 human papil
3	26	26.0	13	12	Q918t6 human papil
4	26	26.0	16	12	Q918u2 human papil
5	26	26.0	16	12	Q918t1 human papil
6	26	26.0	16	12	Q918u8 human papil
7	26	26.0	16	12	Q918u6 human papil
8	26	26.0	16	12	Q918u4 human papil
9	26	26.0	16	12	Q918t9 human papil
10	26	26.0	17	3	Q9C0S9
11	26	26.0	17	3	Q9C0S6
12	26	26.0	17	3	Q8NIJ7
13	26	26.0	17	3	Q8NIJ6
14	26	26.0	17	3	Q9C0S7
15	26	26.0	17	3	Q9C0S8
16	26	26.0	17	3	Q9C1Q8

17	26	26.0	17	3	Q8J168
18	26	26.0	17	3	Q870J0
19	26	26.0	17	3	Q96TQ4
20	26	26.0	17	3	Q94758
21	26	26.0	17	3	Q72885
22	26	26.0	17	3	Q727U6
23	26	26.0	17	3	Q727U5
24	25	25.0	12	5	Q8MY01
25	25	25.0	17	2	Q55091
26	24	24.0	13	11	O54809
27	24	24.0	16	11	Q9ERP8
28	24	24.0	17	2	Q9P581
29	23	23.0	12	13	Q9P867
30	23	23.0	14	4	Q16332
31	23	23.0	16	5	Q9TWS1
32	23	23.0	16	6	O77491
33	22	22.0	11	7	O77872
34	22	22.0	11	7	O77873
35	22	22.0	11	7	O77871
36	22	22.0	14	2	Q9R5Q9
37	22	22.0	14	4	Q16484
38	22	22.0	16	12	Q84055
39	21.5	21.5	15	13	Q8AXO9
40	21	21.0	12	12	Q85666
41	21	21.0	13	6	Q9GUJ2
42	21	21.0	13	11	Q9QV13
43	21	21.0	13	13	P82821
44	21	21.0	13	13	P82822
45	21	21.0	14	2	Q43905

#### ALIGNMENTS

RESULT 1

Q8QZ5	PRELIMINARY;	PRT;	13 AA.
AC	O8QZ5		
DT	O1-JUN-2002 (TRENBLrel. 21, Created)		
DT	O1-JUN-2002 (TRENBLrel. 21, Last sequence update)		
DT	O1-JUN-2003 (TRENBLrel. 24, Last annotation update)		
DE	Guanine nucleotide binding protein (Fragment).		
GN	GNAO.		
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;		
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;		
OC	Tetraodontidae; Tetraodontidae; Takifugu.		
OX	NCBI_TaxID=31033;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=97129408; PubMed=8973916;		
RA	Sarwal M.M., Sontag J.M., Hoang L., Brenner S., Wilkie T.M.;		
RT	"G protein alpha subunit multigene family in the Japanese puffer fish		
RL	Genome Res. 6:1207-1215 (1996).		
DR	EMBL; L79891; AAL77640.1; -		
DR	GO; GO:0004871; F:signal transducer activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.		
DR	InterPro; IPR001019; Gprotein_alpha.		
DR	Pfam; PF00503; G-alpha; 1.		
FT	NON_TER 1 1		
FT	NON_TER 13 13		
SQ	SEQUENCE 13 AA; 1336 MW; 465B59640B44B5B3 CRC64;		

Query Match 27.0%; Score 27; DB 13; Length 13;

Best Local Similarity 75.0%; Pred. No. 7e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ASELGKST 9

Db 1 AGESGKST 8

```

RESULT 2
Q918T4 ID Q918T4 PRELIMINARY; PRT; 13 AA.
AC Q918T4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC7;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407220; AAL01406.1; -.
FT NON_TER 1
FT SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;
SQ

Query Match 26.0%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 3
Q918T6 ID Q918T6 PRELIMINARY; PRT; 13 AA.
AC Q918T6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407219; AAL01403.1; -.
FT NON_TER 1
FT SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;
SQ

Query Match 26.0%; Score 26; DB 12; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 4 CVS--GQNTNT 12

RESULT 4
Q918U2 ID Q918U2 PRELIMINARY; PRT; 16 AA.
AC Q918U2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)

```

```

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC4;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407217; AAL01397.1; -.
FT NON_TER 1
FT SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;
SQ

Query Match 26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 7 CVS--GQNTNT 15

RESULT 5
Q918T1 ID Q918T1 PRELIMINARY; PRT; 16 AA.
AC Q918T1;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC8;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF407221; AAL01409.1; -.
FT NON_TER 1
FT SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;
SQ

Query Match 26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 CASELGKSTNT 11
DB 7 CVS--GQNTNT 15

RESULT 6
Q918U8 ID Q918U8 PRELIMINARY; PRT; 16 AA.
AC Q918U8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;

```

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=HPV16E2CC1;
RA  Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT  "Sequence variation and physical state of human Papillomavirus type 16
RL  cervical cancer isolates from Australia and New Caledonia.";
DR  Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
FT  EMBL; AF407214; AAL01388.1; -.
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 7
Q918U6 ID Q918U6 PRELIMINARY; PRT; 16 AA.
AC Q918U6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC2;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
DR EMBL; AF407215; AAL01391.1; -.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 8
Q918U4 ID Q918U4 PRELIMINARY; PRT; 16 AA.
AC Q918U4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC3;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
DR Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

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DR  EMBL; AF407216; AAL01394.1; -.
FT  NON_TER 1
SQ  SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 9
Q918T9 ID Q918T9 PRELIMINARY; PRT; 16 AA.
AC Q918T9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE E1 protein (Fragment).
GN E1.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E2CC5;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human Papillomavirus type 16
RL cervical cancer isolates from Australia and New Caledonia.";
DR EMBL; AF407218; AAL01400.1; -.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match      26.0%; Score 26; DB 12; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY  1 CASELGKSTNT 11
Db  | | | | |
    7 CVS--GQNTNT 15

RESULT 10
Q9C0S9 ID Q9C0S9 PRELIMINARY; PRT; 17 AA.
AC Q9C0S9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E1-alpha (Fragment).
GN TEF1.
OS Claviceps purpurea (Ergot fungus).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX NCBI_TaxID=5111;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Clp-1, and Clp-2;
RA Toolley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA Koolau G.A.;
RT "Characterization of Claviceps species pathogenic on sorghum by
RL sequence analysis of the beta-tubulin gene intron 3 region and E1-
RL alpha gene intron 4.";
DR Mycologia 93:541-551(2001).
DR EMBL; AF255889; AAK37634.1; -.
DR EMBL; AF255890; AAK37635.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

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Query Match 26.0%; Score 26; DB 3; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9  
 :|||||:  
 Db 8 AELGKGS 15

## RESULT 11

Q9C0S6 PRELIMINARY; PRT; 17 AA.  
 AC Q9C0S6;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE EFl-alpha (Fragment).  
 GN TEFL.  
 OS Claviceps africana.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.  
 OX NCBI\_TaxID=83212;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=Cla-2, Cla-7, Cla-1, and Cla-2;  
 RA Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,  
 RA Kulda G.A.;  
 RA "Characterization of Claviceps species pathogenic on sorghum by  
 RT sequence analysis of the beta-tubulin gene intron 3 region and EFl-  
 RT alpha gene intron 4.";  
 RL Mycologia 93:541-551(2001).  
 DR EMBL; AF255896; AAK37641.1; -  
 DR EMBL; AF255897; AAK37642.1; -  
 DR EMBL; AF255898; AAK37643.1; -  
 DR EMBL; AF255899; AAK37644.1; -  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match 26.0%; Score 26; DB 3; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9  
 :|||||:  
 Db 8 AELGKGS 15

## RESULT 12

Q8NIJ7 PRELIMINARY; PRT; 17 AA.  
 AC Q8NIJ7;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Translation elongation factor 1 alpha (fragment).  
 OS Fusarium solani.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=169388;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=T-8, 3-bean, and 71-tomato;  
 RA Li S.;  
 RA "Molecular characterization of Fusarium solani isolates based on the  
 RT translation elongation factor 1 alpha gene.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY043480; AAK95394.1; -  
 DR EMBL; AY043481; AAK95395.1; -  
 DR EMBL; AY043482; AAK95396.1; -  
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
 KW Elongation factor.

FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match 26.0%; Score 26; DB 3; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9  
 :|||||:  
 Db 8 AELGKGS 15

## RESULT 13

Q8NIJ6 PRELIMINARY; PRT; 17 AA.  
 ID Q8NIJ6;  
 AC Q8NIJ6;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
 DE Translation elongation factor 1-alpha (fragment).  
 OS Fusarium solani f. sp. glycines.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
 OX NCBI\_TaxID=108887;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RC STRAIN=Various strains;  
 RA Li S.;  
 RA "Molecular characterization of Fusarium solani f. sp. glycines based  
 RT on the translation elongation factor 1-alpha gene.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF395645; AAM73735.1; -  
 DR EMBL; AF395646; AAM73736.1; -  
 DR EMBL; AF395647; AAM73737.1; -  
 DR EMBL; AF395648; AAM73738.1; -  
 DR EMBL; AF395649; AAM73739.1; -  
 DR EMBL; AF395650; AAM73740.1; -  
 DR EMBL; AF395651; AAM73741.1; -  
 DR EMBL; AF395652; AAM73742.1; -  
 DR EMBL; AF395653; AAM73743.1; -  
 DR EMBL; AF395654; AAM73744.1; -  
 DR EMBL; AF395655; AAM73745.1; -  
 DR EMBL; AF395656; AAM73746.1; -  
 DR EMBL; AF395657; AAM73747.1; -  
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.  
 KW Elongation factor.  
 FT NON\_TER 1  
 FT NON\_TER 17  
 SQ SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match 26.0%; Score 26; DB 3; Length 17;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+03;  
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASELGKST 9  
 :|||||:  
 Db 8 AELGKGS 15

## RESULT 14

Q9C0S7 PRELIMINARY; PRT; 17 AA.  
 ID Q9C0S7;  
 AC Q9C0S7;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE EFl-alpha (fragment).  
 GN TEFL.  
 OS Claviceps sorghicola.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.  
 OX NCBI\_TaxID=83213;

```

RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Cjap-2, and Cjap-4;
RA  Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA  Kuldau G.A.;
RT  "Characterization of Claviceps species pathogenic on sorghum by
RT  sequence analysis of the beta-tubulin gene intron 3 region and EF1-
RT  alpha gene intron 4."
RL  Mycologia 93:541-551(2001).
DR  EMBL; AF255894; AAK37639.1; -.
DR  EMBL; AF255895; AAK37640.1; -.
FT  NON_TER 1
FT  NON_TER 17
SQ  SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 ASELGKST 9
Db  8 AAELGKGS 15

RESULT 15
Q9C0S8
ID  Q9C0S8      PRELIMINARY;      PRT;      17 AA.
AC  Q9C0S8;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  EF1-alpha (Fragment).
GN  TEF1.
OS  Claviceps paspali (paspalum straggers ergot).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC  Hypocreomycetidae; Hypocreales; Clavicipitaceae; Claviceps.
OX  NCBI_TaxID=4601;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Cpas-1, and Cpas-2;
RA  Tooley P.W., Goley E.D., Carras M.M., Frederick R.D., Weber E.L.,
RA  Kuldau G.A.;
RT  "Characterization of Claviceps species pathogenic on sorghum by
RT  sequence analysis of the beta-tubulin gene intron 3 region and EF1-
RT  alpha gene intron 4."
RL  Mycologia 93:541-551(2001).
DR  EMBL; AF255892; AAK37637.1; -.
DR  EMBL; AF255893; AAK37638.1; -.
FT  NON_TER 1
FT  NON_TER 17
SQ  SEQUENCE 17 AA; 1911 MW; 110075F1817FF1D9 CRC64;

Query Match      26.0%; Score 26; DB 3; Length 17;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  2 ASELGKST 9
Db  8 AAELGKGS 15

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Search completed: September 5, 2004, 10:56:03  
Job time : 58 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:48:30 ; Search time 62 seconds  
(without alignments)  
77.473 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCRPPC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 470470

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	17	AAU04527	AAU04527 VEGF base
2	97	97.0	17	AAU04550	AAU04550 VEGF base
3	97	97.0	17	AAU04546	AAU04546 VEGF base
4	93	93.0	17	AAU04547	AAU04547 VEGF base
5	93	93.0	17	AAU04551	AAU04551 VEGF base
6	93	93.0	17	AAU04549	AAU04549 VEGF base
7	89	89.0	17	AAU04548	AAU04548 VEGF base
8	72	72.0	13	AAU04524	AAU04524 VEGF base
9	69	69.0	13	AAU04534	AAU04534 VEGF base
10	65	65.0	13	AAU04535	AAU04535 VEGF base
11	65	65.0	13	AAU04537	AAU04537 VEGF base
12	61	61.0	13	AAU04536	AAU04536 VEGF base
13	48	48.0	14	AAU04542	AAU04542 VEGF base
14	39	39.0	8	AAU08482	AAU08482 Peptide #
15	37	37.0	10	AAU10122	AAU10122 Peptide #
16	37	37.0	12	AAU57039	AAU57039 Feline im
17	35	35.0	17	AAU93529	AAU93529 PKC seque
18	33	33.0	16	AAU95280	AAU95280 Human ser
19	32	32.0	9	AAU98568	AAU98568 Human TAD
20	32	32.0	11	AAU46652	AAU46652 HIV-1 Tat
21	32	32.0	12	AAU43828	AAU43828 HIV-1 Tat
22	32	32.0	12	AAU11133	AAU11133 HIV-1 Tat
23	32	32.0	12	AAU52574	AAU52574 Cyclic pe
24	32	32.0	12	AAU24778	AAU24778 HIV-1 Tat
25	32	32.0	12	AAU17381	AAU17381 Antimicro

#### RESULT 1

AAU04527 ID AAU04527 standard; protein; 17 AA.

XX AC AAU04527;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #1.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX KW neovascularisation; lymphangiogenesis; psoriasis; tumour;

XX KW diabetes induced neovascular sequelae; rheumatoid arthritis;

XX KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and

FT residue 17 of an identical peptide to form a dimeric peptide, or to residue 1 of the sequence appearing as AAU04528, also forming a dimeric peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US0001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis, or lymphangiogenesis, is produced by cyclizing a peptide loop fragment from an exposed loop of a growth factor protein by oxidizing the cysteine residues.

XX Claim 59; Page 32; 102pp; English.

#### ALIGNMENTS

26	32	32.0	12	4	AAU46653	AAU46653 HIV-1 Tat
27	32	32.0	13	4	AAU46654	AAU46654 HIV-1 Tat
28	32	32.0	13	4	AAU08459	AAU08459 Peptide C
29	32	32.0	13	5	ABJ04094	ABJ04094 Immunoglob
30	32	32.0	14	3	AAU66872	AAU66872 T cell an
31	32	32.0	14	4	AAU46655	AAU46655 HIV-1 Tat
32	32	32.0	15	4	AAU46656	AAU46656 HIV-1 Tat
33	32	32.0	15	4	ABP24824	ABP24824 HIV DR su
34	32	32.0	15	6	ABR81834	ABR81834 HIV Tat T
35	32	32.0	16	2	AAU25715	AAU25715 CB1 parti
36	32	32.0	16	2	AAU57342	AAU57342 Peptide f
37	32	32.0	16	2	AAU14288	AAU14288 Citrus dl
38	32	32.0	16	3	AAU66903	AAU66903 T cell an
39	32	32.0	16	4	AAU46657	AAU46657 HIV-1 Tat
40	32	32.0	16	5	ABR88471	ABR88471 C aulicus
41	32	32.0	16	6	ABR81821	ABR81821 HIV Tat r
42	32	32.0	17	3	AAU25943	AAU25943 Pl mimoto
43	32	32.0	17	3	AAU26024	AAU26024 Human IGE
44	32	32.0	17	4	AAU46658	AAU46658 HIV-1 Tat
45	32	32.0	17	4	AAU16668	AAU16668 Peptide #

CC The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 100; DB 4; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-08; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0;

QY 1 CASELGKSTNTFCCKPPC 17  
 DB 1 CASELGKSTNTFCCKPPC 17  
 |||||

RESULT 2  
 AAU04550  
 ID AAU04550 standard; peptide; 17 AA.

XX AC AAU04550;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #7.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17

FT /note= "A disulfide bond forms between residue 17 and  
 residue 1 of the sequence appearing as AAU04528, forming  
 a dimeric peptide"

XX PN WC200152875-A1.

XX PD 26-JUL-2001.

XX XX 18-JAN-2001; 2001WO-US001533.

XX XX 18-JAN-2000; 2000US-0176293P.

XX PR 16-MAY-2000; 2000US-0204590P.

XX

PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX DR WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.

XX Example 25; Page 49; 102pp; English.

PS The sequence represents a dimeric bicyclic peptide of the invention,  
 XX whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 17 AA;

Query Match 97.0%; Score 97; DB 4; Length 17;

Best Local Similarity 94.1%; Pred. No. 1.7e-07;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCCKPPC 17

DB 1 CASELGKSTNTFCCKPPC 17

RESULT 3

AAU04546

ID AAU04546 standard; peptide; 17 AA.

XX AC AAU04546;

XX DT 26-SEP-2001 (first entry)

XX DE VEGF based bicyclic dimeric peptide #3.

XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Disulfide-bond 1..13 /note= "This bond cyclises the peptide"

FT Disulfide-bond 17



FT /note= "A disulfide bond forms between residue 17 and  
 FT residue 17 of an identical peptide to form a dimeric  
 FT peptide"  
 XX  
 PN W0200152875-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 18-JAN-2001; 2001WO-US001533.  
 XX  
 PR 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX WPI; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 PS Example 26; Page 49; 102pp; English.  
 XX  
 CC The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclizing the peptide by oxidizing the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 17 AA;  
 Query Match 97.0%; Score 97; DB 4; Length 17;  
 Best Local Similarity 94.1%; Pred. No. 1.7e-07;  
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CASLGLKSTNTFCPPC 17  
 ||:|||||||  
 Db 1 CATELGLKSTNTFCPPC 17  
 RESULT 4  
 AAU04547  
 ID AAU04547 standard; peptide; 17 AA.  
 AC AAU04547;  
 XX  
 XX 26-SEP-2001 (first entry)  
 DT  
 XX

DE VEGF based bicyclic dimeric peptide #4.  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1..13  
 FT /note= "This bond cyclises the peptide"  
 FT Disulfide-bond 17  
 FT /note= "A disulfide bond forms between residue 17 and  
 FT residue 17 of an identical peptide to form a dimeric  
 FT peptide"  
 XX  
 PN W0200152875-A1.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 18-JAN-2001; 2001WO-US001533.  
 XX  
 PR 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX  
 PA (LUDW-) LUDWIG INST CANCER RES.  
 XX  
 PI Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX WPI; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 PS Example 26; Page 49; 102pp; English.  
 XX  
 CC The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclizing the peptide by oxidizing the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 17 AA;  
 Query Match 93.0%; Score 93; DB 4; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 6.9e-07;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CASELGKSTNTFCRPPC 17  
 DB 1 CASELGKSTNTFCRPPC 17

RESULT 5  
 AAU04551  
 ID AAU04551 standard; peptide; 17 AA.  
 XX AAU04551;  
 AC AAU04551;  
 XX AAU04551;  
 DT 26-SEP-2001 (first entry)  
 XX VEGF based bicyclic dimeric peptide #8.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX Synthetic.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Disulfide-bond 1..13 /note= "This bond cyclises the peptide"  
 FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and  
 residue 1 of the sequence appearing as AAU04528, forming  
 a dimeric peptide"  
 FT WO200152875-A1.  
 PN 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 from an exposed loop of a growth factor protein by oxidizing the cysteine  
 residues.  
 XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,  
 whose 3-dimensional structure is modelled on the expose loop of human  
 VEGFD (vascular endothelial growth factor). The invention relates to a  
 method of producing a monomeric monocyclic peptide by a measuring beta-  
 beta carbon separation distances on opposite antiparallel strands of a  
 peptide loop fragment from an exposed loop of a growth factor protein and  
 cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 peptides) and a cyclic peptide with at least one amino acid deleted prior  
 to cyclisation are used to interfere with angiogenesis,  
 neovascularisation or lymphangiogenesis in a mammal with a condition  
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

or brain. The peptides are used to image blood vessels and lymphatic  
 vasculature. The monomeric and bicyclic peptides are used to interfere  
 with at least one biological activity induced by VEGF, VEGF-C or -D and  
 are also used in combination with an anti-inflammatory agent, to treat a  
 chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 diabetic retinopathy

XX Sequence 17 AA;  
 SQ Query Match 93.0%; Score 93; DB 4; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 6.9e-07;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CASELGKSTNTFCRPPC 17  
 DB 1 CASELGRSTNSFCRPPC 17

RESULT 6  
 AAU04549  
 ID AAU04549 standard; peptide; 17 AA.  
 XX AAU04549;  
 AC AAU04549;  
 XX 26-SEP-2001 (first entry)  
 XX VEGF based bicyclic dimeric peptide #6.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX Synthetic.  
 OS Synthetic.

XX Key Location/Qualifiers  
 FH Disulfide-bond 1..13 /note= "This bond cyclises the peptide"  
 FT Disulfide-bond 17 /note= "A disulfide bond forms between residue 17 and  
 residue 17 of an identical peptide to form a dimeric  
 peptide"  
 FT WO200152875-A1.  
 PN 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 from an exposed loop of a growth factor protein by oxidizing the cysteine  
 residues.  
 XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,  
 whose 3-dimensional structure is modelled on the expose loop of human  
 VEGFD (vascular endothelial growth factor). The invention relates to a  
 method of producing a monomeric monocyclic peptide by a measuring beta-  
 beta carbon separation distances on opposite antiparallel strands of a  
 peptide loop fragment from an exposed loop of a growth factor protein and  
 cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 peptides) and a cyclic peptide with at least one amino acid deleted prior  
 to cyclisation are used to interfere with angiogenesis,  
 neovascularisation or lymphangiogenesis in a mammal with a condition  
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,

CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 17 AA;

Query Match 93.0%; Score 93; DB 4; Length 17;  
 Best Local Similarity 88.2%; Pred. No. 6.9e-07;  
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17  
 |||||:||||:|||||  
 Db 1 CASELGRSTNSFCPPC 17

RESULT 7  
 AAU04548  
 ID AAU04548 standard; peptide; 17 AA.  
 AC  
 XX AAU04548;

DT 26-SEP-2001 (first entry)

DE VEGF based bicyclic dimeric peptide #5.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 1..13

FT Disulfide-bond 17 /note= "This bond cyclises the peptide"

FT /note= "A disulfide bond forms between residue 17 and  
 residue 17 of an identical peptide to form a dimeric  
 peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment

PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.

XX Example 26; Page 49; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX

SQ Sequence 17 AA;

Query Match 89.0%; Score 89; DB 4; Length 17;  
 Best Local Similarity 82.4%; Pred. No. 2.7e-06;  
 Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17  
 |||||:||||:|||||

Db 1 CASDVGKSTNTWCKPPC 17

RESULT 8

AAU04524

ID AAU04524 standard; peptide; 13 AA.

AC AAU04524;

DT 26-SEP-2001 (first entry)

DE VEGF based monocyclic peptide 1.

KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.

FH Key Location/Qualifiers

FT Disulfide-bond 1..13

FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

Sun Sep 5 11:41:18 2004

XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 DR or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine  
 XX residues.  
 PS Claim 49; Page 32; 102pp; English.  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX Sequence 13 AA;  
 SQ Query Match 69.0%; Score 69; DB 4; Length 13;  
 Best Local Similarity 92.3%; Pred. No. 0.002; Gaps 0;  
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CASELGKSTNTFC 13  
 Db 1 CASELGKSTNTFC 13  
 RESULT 10  
 AAU04535  
 ID AAU04535 standard; peptide; 13 AA.  
 XX AAU04535;  
 AC AAU04535;  
 XX 26-SEP-2001 (first entry)  
 DT VEGF based monocyclic peptide 13.  
 DE Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW VEGF based monocyclic peptide 13.  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;

XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 DR or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine  
 XX residues.  
 PS Claim 49; Page 32; 102pp; English.  
 XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX Sequence 13 AA;  
 SQ Query Match 72.0%; Score 72; DB 4; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 0.00073;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CASELGKSTNTFC 13  
 Db 1 CASELGKSTNTFC 13  
 RESULT 9  
 AAU04534  
 ID AAU04534 standard; peptide; 13 AA.  
 XX AAU04534;  
 AC AAU04534;  
 XX 26-SEP-2001 (first entry)  
 DT VEGF based monocyclic peptide 12.  
 DE Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX Synthetic.  
 OS Key Location/Qualifiers  
 FH Disulfide-bond 1..13  
 FT /note= "This bond cyclises the peptide"

KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX

OS Synthetic.

XX Key Location/Qualifiers  
 XX Disulfide-bond 1. 13  
 FT /note= "This bond cyclises the peptide"

XX WO200152875-A1.

XX 26-JUL-2001.

XX 18-JAN-2001; 2001WO-US001533.

XX 18-JAN-2000; 2000US-0176293P.

XX 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

XX Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX WPI; 2001-442248/47.

XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 XX from an exposed loop of a growth factor protein by oxidizing the cysteine  
 XX residues.

XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the exposed loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascular sequelae, or chronic liver  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascularisation of the liver, excessive  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy

XX Sequence 13 AA;

Query Match 65.0%; Score 65; DB 4; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 0.008;  
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTWFC 13

|||||:||||

Db 1 CASELGKSTWFC 13

RESULT 11

AAU04537

ID

XX

AC

XX

XX

DT

XX

DE

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KW

KW

KW

KW

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AAU04537 standard; peptide; 13 AA.

AAU04537;

26-SRP-2001 (first entry)

VEGF based monocyclic peptide 15.

Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 diabetes induced neovascular sequelae; rheumatoid arthritis;  
 diabetic retinopathy; chronic inflammation; cyclic.

Synthetic.

Key Location/Qualifiers  
 Disulfide-bond 1. 13  
 /note= "This bond cyclises the peptide"

WO200152875-A1.

26-JUL-2001.

18-JAN-2001; 2001WO-US001533.

18-JAN-2000; 2000US-0176293P.

16-MAY-2000; 2000US-0204590P.

(LUDW-) LUDWIG INST CANCER RES.

Achen MG, Hughes RA, Stacker S, Cendron A;

WPI; 2001-442248/47.

Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 from an exposed loop of a growth factor protein by oxidizing the cysteine  
 residues.

Example 25; Page 47; 102pp; English.

The sequence represents a monomeric monocyclic peptide of the invention,  
 whose 3-dimensional structure is modelled on the exposed loop of human  
 VEGFD (vascular endothelial growth factor). The invention relates to a  
 method of producing a monomeric monocyclic peptide by a measuring beta-  
 beta carbon separation distances on opposite antiparallel strands of a  
 peptide loop fragment from an exposed loop of a growth factor protein and  
 cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 peptides) and a cyclic peptide with at least one amino acid deleted prior  
 to cyclisation are used to interfere with angiogenesis,  
 neovascularisation or lymphangiogenesis in a mammal with a condition  
 characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 The condition is diabetic retinopathy, psoriasis, arthropathy,  
 hemangioma, vascularised malignant or benign tumour, post-recovery  
 cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 trauma, substance-induced neovascularisation of the liver, excessive  
 hormone-related angiogenic dysfunction, diabetes induced neovascular  
 sequelae, hypertension induced neovascularisation of the liver, excessive  
 infection. The peptides are also used to modulate vascular permeability  
 in a mammal (the mammal has a condition characterised by fluid  
 accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 or brain. The peptides are used to image blood vessels and lymphatic  
 vasculature. The monomeric and bicyclic peptides are used to interfere  
 with at least one biological activity induced by VEGF, VEGF-C or -D and  
 are also used in combination with an anti-inflammatory agent, to treat a  
 chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 diabetic retinopathy

Sequence 13 AA;

Query Match 65.0%; Score 65; DB 4; Length 13;  
 Best Local Similarity 84.6%; Pred. No. 0.008;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
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Db 1 CASELGKSTNTSFC 13

RESULT 12  
AAU04536  
ID AAU04536 standard; peptide; 13 AA.

XX AAU04536;  
AC AAU04536;

DT 26-SEP-2001 (first entry)

XX VEGF based monocyclic peptide 14.

DE Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.  
XX Synthetic.  
OS

XX Key Location/Qualifiers  
FH Disulfide-bond 1..13  
FT /note= "This bond cyclises the peptide"  
XX WO200152875-A1.  
XX 26-JUL-2001.  
XX 18-JAN-2001; 2001WO-US001533.  
XX 18-JAN-2000; 2000US-0176293P.  
XX 16-MAY-2000; 2000US-0204590P.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX Achen MG, Hughes RA, Stacker S, Cendron A;  
XX WPI; 2001-442248/47.  
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
PT residues.  
XX Example 25; Page 47; 102pp; English.

XX The sequence represents a monomeric monocyclic peptide of the invention,  
CC whose 3-dimensional structure is modelled on the exposed loop of human  
CC VEGF (vascular endothelial growth factor). The invention relates to a  
CC method of producing a monomeric monocyclic peptide by a measuring beta-  
CC beta carbon separation distances on opposite antiparallel strands of a  
CC peptide loop fragment from an exposed loop of a growth factor protein and  
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
CC to cyclisation are used to interfere with angiogenesis,  
CC neovascularisation or lymphangiogenesis in a mammal with a condition  
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
CC hemangioma, vascularised malignant or benign tumour, post-recovery  
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
CC trauma, substance-induced neovascularisation of the liver, excessive  
CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
CC infection. The peptides are also used to modulate vascular permeability  
CC in a mammal (the mammal has a condition characterised by fluid  
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
CC or brain. The peptides are used to image blood vessels and lymphatic  
CC vasculature. The monomeric and bicyclic peptides are used to interfere

CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
CC are also used in combination with an anti-inflammatory agent, to treat a  
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
CC diabetic retinopathy  
XX SQ Sequence 13 AA;  
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QY 1 CASELGKSTNTFC 13  
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Db 1 CASDVGKSTNTWC 13

RESULT 13  
AAU08482  
ID AAU08482 standard; peptide; 14 AA.

XX AAU08482;  
AC AAU08482;

DT 21-NOV-2001 (first entry)

XX Peptide #4 inhibiting human VEGF-C mediated activation of VEGFR-3.

DE Human; vascular endothelial growth factor; VEGF-C; vasculogenesis;  
KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;  
KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;  
KW VEGFR-3.  
XX Homo sapiens.  
OS

XX Key Location/Qualifiers  
FH Misc-difference 13..13  
FT /note= "Any amino acid"  
XX WO200162942-A2.  
XX 30-AUG-2001.  
XX 26-FEB-2001; 2001WO-US006113.  
XX 25-FEB-2000; 2000US-0185205P.  
XX 18-MAY-2000; 2000US-0205331P.  
XX (LUDW-) LUDWIG INST CANCER RES.  
XX (LICN) LICENTIA OF.  
XX Alitalo K, Jeltsch MW;  
XX WPI; 2001-536640/59.  
XX Polypeptides that bind cellular receptors for vascular endothelial growth  
PT factors, polynucleotides encoding them.  
XX Claim 65; Page 147; 261pp; English.

XX The present invention relates to polypeptides that bind cellular  
CC receptors for vascular endothelial growth factors (VEGFs), the  
CC polynucleotides encoding them, and their use for identifying agents that  
CC modulate interactions between VEGFs and their receptors. VEGFs and their  
CC receptors play an important role in vasculogenesis, the development of  
CC the embryonic vasculature from early differentiating endothelial cells  
CC and angiogenesis, the process of forming new blood vessels from pre-  
CC existing ones. Modulators of interactions between VEGF and its receptors  
CC may be used to treat dysfunction of the endothelial cell regulatory  
CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid  
CC proliferative retinopathies, age-related macular degeneration, rheumatoid  
CC arthritis and psoriasis. The polypeptides of the invention exhibit unique  
CC receptor binding profiles compared to known naturally occurring VEGFs.  
CC AAU08479-AAU08483 represents peptides which inhibit human VEGF-C mediated  
CC activation of VEGFR-3

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XX SQ Sequence 14 AA;
Query Match 48.0%; Score 48; DB 4; Length 14;
Best Local Similarity 88.9%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TNTFCPPC 17
Db 1 TNTFFKPPC 9
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1 TNTFFKPPC 9

RESULT 14
AAU08481
ID AAU08481 standard; peptide; 8 AA.
XX AC AAU08481;
XX AC AAU08481;
XX DT 21-NOV-2001 (first entry)
XX DE Peptide #3 inhibiting human VEGF-C mediated activation of VEGFR-3.
XX OS Homo sapiens.
XX KW Human; vascular endothelial growth factor; VEGF-C; vasculogenesis;
XX KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;
XX KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;
XX KW VEGFR-3.
XX OS Homo sapiens.
XX PN WO200162942-A2.
XX PD 30-AUG-2001.
XX PF 26-FEB-2001; 2001WO-US006113.
XX PR 25-FEB-2000; 2000US-0185205P.
XX PR 18-MAY-2000; 2000US-0205331P.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PA (LICN) LICENTIA OY.
XX PI Alitalo K, Jeltsch MM;
XX WPI; 2001-536640/59.
XX PT Polypeptides that bind cellular receptors for vascular endothelial growth
XX PT factors, polynucleotides encoding them.
XX PS Claim 64; Page 147; 261pp; English.
XX CC The present invention relates to polypeptides that bind cellular
XX CC receptors for vascular endothelial growth factors (VEGFs), the
XX CC polynucleotides encoding them, and their use for identifying agents that
XX CC modulate interactions between VEGFs and their receptors. VEGFs and their
XX CC receptors play an important role in vasculogenesis, the development of
XX CC the embryonic vasculature from early differentiating endothelial cells
XX CC and angiogenesis, the process of forming new blood vessels from pre-
XX CC existing ones. Modulators of interactions between VEGF and its receptors
XX CC may be used to treat dysfunction of the endothelial cell regulatory
XX CC system. Such disorders include cancers, abnormal angiogenesis,
XX CC proliferative retinopathies, age-related macular degeneration, rheumatoid
XX CC arthritis and psoriasis. The polypeptides of the invention exhibit unique
XX CC receptor binding profiles compared to known naturally occurring VEGFs.
XX CC AAU08479-AAU08483 represents peptides which inhibit human VEGF-C mediated
XX CC activation of VEGFR-3
XX SQ Sequence 8 AA;
Query Match 39.0%; Score 39; DB 4; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TNTFCPPC 16

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Db 1 TNTFFKPP 8
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1 TNTFFKPP 8

RESULT 15
AAW10122
ID AAW10122 standard; protein; 10 AA.
XX AC AAW10122;
XX AC AAW10122;
XX DT 18-SEP-1997 (first entry)
XX DE Human agouti signalling protein fragment #10.
XX KW Agouti signalling protein; ASP; depigmenting activity; cosmetic;
XX KW hyperpigmentary condition; melasma photoageing spots; solar keratosis;
XX KW post-inflammatory hyperpigmentation; wound healing; eumelanogenesis;
XX KW vitiligo; leucoderma; albinism; hair greying.
XX OS Homo sapiens.
XX PN WO9700892-A2.
XX PD 09-JAN-1997.
XX PF 21-JUN-1996; 96WO-US010695.
XX PR 23-JUN-1995; 95US-0000436P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Hearing VJ;
XX WPI; 1997-087323/08.
XX PT New agouti signal protein peptide(s) and nucleic acids - used for
XX PT altering melanin prodn., for treating e.g. melasma photo-ageing spots,
XX PT solar keratosis or vitiligo.
XX PS Claim 26; Page 12; 67pp; English.
XX CC The sequences given in AAW10101-29 are biologically active peptides and
XX CC fragments of the agouti signalling protein (ASP) which have depigmenting
XX CC activity. These peptides are useful for cosmetic purposes and for
XX CC clinical application in the prevention or treatment of various
XX CC hyperpigmentary conditions and diseases such as melasma photoageing
XX CC spots, solar keratosis, and post-inflammatory hyperpigmentation such as
XX CC occurs at sites of wound healing. They can also be used to provide
XX CC enhanced eumelanogenesis for treating eg. vitiligo, leucoderma, some
XX CC forms of albinism and hair greying
XX SQ Sequence 10 AA;
Query Match 37.0%; Score 37; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 STNTFCPP 16
Db 1 ATNDSCKPP 9
|||||
1 ATNDSCKPP 9

Search completed: September 5, 2004, 10:54:38
Job time : 63 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:56:07; Search time 66 Seconds  
(without alignments)  
81.153 Million cell updates/sec

Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCPPC 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 230634

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pcp:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pcp:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pcp:\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pcp:\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pcp:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pcp:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pcp:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	100	100.0	17	9	US-09-761-636A-8
2	97	97.0	17	9	US-09-761-636A-27
3	97	97.0	17	9	US-09-761-636A-31
4	93	93.0	17	9	US-09-761-636A-28
5	93	93.0	17	9	US-09-761-636A-30
6	93	93.0	17	9	US-09-761-636A-32
7	89	89.0	17	9	US-09-761-636A-29
8	72	72.0	13	9	US-09-761-636A-5
9	69	69.0	13	9	US-09-761-636A-15
10	65	65.0	13	9	US-09-761-636A-16
11	65	65.0	13	9	US-09-761-636A-17
12	61	61.0	13	9	US-09-761-636A-18
13	37	37.0	10	12	US-10-435-238-22
14	32	32.0	7	9	US-09-805-761-61
15	32	32.0	7	9	US-09-805-761-63

16 32 32.0 9 16 US-10-600-187-78 Sequence 78, Appl  
17 32 32.0 12 14 US-10-247-946-4 Sequence 4, Appl  
18 32 32.0 12 14 US-10-251-526-4 Sequence 4, Appl  
19 32 32.0 13 9 US-09-795-006A-141 Sequence 141, Appl  
20 32 32.0 13 9 US-10-415-665-14 Sequence 14, Appl  
21 32 32.0 16 10 US-09-910-009A-454 Sequence 454, Appl  
22 32 32.0 17 12 US-10-362-527-115 Sequence 115, Appl  
23 32 32.0 17 12 US-10-362-527-115 Sequence 156, Appl  
24 31 31.0 10 9 US-09-779-308-461 Sequence 461, Appl  
25 31 31.0 11 12 US-10-435-238-21 Sequence 21, Appl  
26 31 31.0 11 12 US-09-784-553C-58 Sequence 58, Appl  
27 31 31.0 11 15 US-10-209-201C-58 Sequence 58, Appl  
28 31 31.0 15 10 US-09-932-613-67 Sequence 67, Appl  
29 31 31.0 15 10 US-09-932-322-67 Sequence 67, Appl  
30 31 31.0 16 9 US-09-777-710A-4 Sequence 4, Appl  
31 31 31.0 16 10 US-09-992-665-35 Sequence 35, Appl  
32 31 31.0 17 9 US-09-944-849-11 Sequence 11, Appl  
33 30 30.0 10 14 US-10-208-304-14 Sequence 14, Appl  
34 30 30.0 12 10 US-09-954-385-335 Sequence 335, Appl  
35 30 30.0 14 10 US-09-792-686A-10 Sequence 10, Appl  
36 30 30.0 14 13 US-10-139-841-9 Sequence 9, Appl  
37 30 30.0 14 13 US-10-014-485A-9 Sequence 9, Appl  
38 30 30.0 14 14 US-10-062-710-38 Sequence 38, Appl  
39 30 30.0 14 14 US-10-174-105A-9 Sequence 9, Appl  
40 30 30.0 15 9 US-09-829-549A-33 Sequence 33, Appl  
41 30 30.0 17 14 US-10-031-874A-158 Sequence 158, Appl  
42 29.5 29.5 17 10 US-09-226-157-26 Sequence 26, Appl  
43 29 29.0 10 10 US-09-833-203-58 Sequence 58, Appl  
44 29 29.0 13 14 US-10-007-521-102 Sequence 102, Appl  
45 29 29.0 13 14 US-10-007-521-104 Sequence 104, Appl

## ALIGNMENTS

RESULT 1  
US-09-761-636A-8  
; Sequence 8, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 8  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-636A-8

Query Match 100.0%; Score 100; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 3.2e-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17  
DB 1 CASELGKSTNTFCPPC 17

RESULT 2  
US-09-761-636A-27  
; Sequence 27, Application US/09761636A  
; Patent No. US20020065218A1

us-09-761-636a-8.closed.rapb

Sun Sep 5 11:41:19 2004

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-27

Query Match          97.0%; Score 97; DB 9; Length 17;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-761-636A-31
; Sequence 31, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-31

Query Match          97.0%; Score 97; DB 9; Length 17;
Best Local Similarity 94.1%; Pred. No. 9.2e-08;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CASELGKSTNTFCCKPPC 17
Db      1 CASELGKSTNTFCCKPPC 17

US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-30

Query Match          93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CASELGKSTNTFCCKPPC 17
Db      1 CASELGKSTNTFCCKPPC 17

RESULT 5
US-09-761-636A-30
; Sequence 30, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-30

Query Match          93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 CASELGKSTNTFCCKPPC 17
Db      1 CASELGKSTNTFCCKPPC 17

RESULT 6
US-09-761-636A-32
; Sequence 32, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293

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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-32

Query Match      93.0%; Score 93; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 3.7e-07;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
Db 1 CASELGRSTNSFCPPC 17

RESULT 7
US-09-761-636A-29
; Sequence 29, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-29

Query Match      89.0%; Score 89; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1.5e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFCPPC 17
Db 1 CASDVGKSTNTWCKPPC 17

RESULT 8
US-09-761-636A-5
; Sequence 5, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-5

Query Match      72.0%; Score 72; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CASELGKSTNTFC 13

RESULT 9
US-09-761-636A-15
; Sequence 15, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-15

Query Match      69.0%; Score 69; DB 9; Length 13;
Best Local Similarity 92.3%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13
Db 1 CATELGKSTNTFC 13

RESULT 10
US-09-761-636A-16
; Sequence 16, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 13
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-16
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Query Match 65.0%; Score 65; DB 9; Length 13;  
Best Local Similarity 84.6%; Pred. No. 0.0049;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
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Db 1 CASELGKSTNTFC 13

RESULT 11  
US-09-761-636A-18  
; Sequence 18, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 18  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-761-636A-18

Query Match 65.0%; Score 65; DB 9; Length 13;  
Best Local Similarity 84.6%; Pred. No. 0.0049;  
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
|||:|||||:  
Db 1 CASELGKSTNTFC 13

RESULT 12  
US-09-761-636A-17  
; Sequence 17, Application US/09761636A  
; Patent No. US20020065218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 17  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: synthetic construct  
US-09-761-636A-17

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Best Local Similarity 76.9%; Pred. No. 0.02;  
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CASELGKSTNTFC 13  
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Db 1 CASELGKSTNTFC 13

RESULT 13  
US-10-435-238-22  
; Sequence 22, Application US/10435238  
; Publication No. US20030224972A1  
; GENERAL INFORMATION:  
; APPLICANT: HEARING, Vincent J., Jr.  
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Needle & Rosenberg, P.C.  
; STREET: 127 Peachtree St., N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30303-1811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/435,238  
; FILING DATE: 08-May-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/983,157  
; FILING DATE: 22-Dec-1997  
; APPLICATION NUMBER: PCT/US96/10695  
; FILING DATE: 21 JUN 1996  
; APPLICATION NUMBER: 60/ 000,436  
; FILING DATE: 23 JUN 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spratt, Gwendolyn D.  
; REGISTRATION/DOCKET NUMBER: 36,016  
; REFERENCE/DOCKET NUMBER: 14014.0195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-9880  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-10-435-238-22

Query Match 37.0%; Score 37; DB 12; Length 10;  
Best Local Similarity 66.7%; Pred. No. 64;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 STNTFCCKPP 16  
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Db 1 ATNDSCKPP 9

RESULT 14  
US-09-805-761-61  
; Sequence 61, Application US/09805761  
; Patent No. US20020165174A1  
; GENERAL INFORMATION:  
; APPLICANT: Gill, Parkesh  
; APPLICANT: Masood, Rizwan  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE  
; TITLE OF INVENTION: VEGF OLIGONUCLEOTIDES  
; FILE REFERENCE: 21327-701CON2

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; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-61

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Query Match          32.0%; Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9  TNTCKP 15
Db      1  TNTCKP 7

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RESULT 15
US-09-805-761-63
; Sequence 63, Application US/09805761
; Patent No. US20020165174A1
; GENERAL INFORMATION:
; APPLICANT: Masood, Rizwan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTISENSE
; FILE REFERENCE: 21327-701CON2
; CURRENT APPLICATION NUMBER: US/09/805,761
; CURRENT FILING DATE: 2001-03-13
; PRIOR APPLICATION NUMBER: PCT/US01/00019
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/487,023
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 2000-11-24
; PRIOR APPLICATION NUMBER: US 09/016,541
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: US 60/037,004
; PRIOR FILING DATE: 1997-01-31
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-761-63

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Query Match          32.0%; Score 32; DB 9; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.2e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      9  TNTCKP 15
Db      1  TNTCKP 7

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Job time : 67 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2004, 10:53:36 ; Search time 20 Seconds  
(without alignments)  
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Title: US-09-761-636A-8

Perfect score: 100

Sequence: 1 CASELGKSTNTFCCKPPC 17

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 157007

Minimum DB seq length: 0

Maximum DB seq length: 17

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pcp.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pcp.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/iaa/6C COMB.pcp.\*
- 6: /cgn2\_6/ptodata/2/iaa/6D COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	37.0	10	4	US-08-983-157B-22
2	32	32.0	9	4	US-09-644-600-78
3	32	32.0	9	4	US-09-654-600A-78
4	32	32.0	12	1	US-08-053-079A-4
5	32	32.0	12	2	US-08-685-589A-228
6	32	32.0	12	4	US-09-462-118-4
7	32	32.0	16	1	US-08-363-566-1
8	31	31.0	10	4	US-08-983-157B-21
9	31	31.0	16	3	US-09-328-501-4
10	31	31.0	16	4	US-09-777-710A-4
11	31	31.0	17	3	US-08-882-046-9
12	31	31.0	17	4	US-09-252-586-19
13	30	30.0	14	2	US-08-443-965B-9
14	30	30.0	14	2	US-08-425-989B-9
15	30	30.0	14	2	US-08-443-966B-9
16	30	30.0	14	3	US-08-853-910-3
17	30	30.0	14	4	US-09-148-712-13
18	29.5	29.5	15	1	US-08-487-485A-4
19	29.5	29.5	17	2	US-08-400-115-26
20	29	29.0	10	2	US-08-637-759B-408
21	29	29.0	10	3	US-08-871-355A-408
22	29	29.0	10	4	US-09-201-945-408
23	29	29.0	10	5	PCT-US96-01735-3
24	29	29.0	13	3	US-08-651-136C-102
25	29	29.0	13	3	US-08-651-136C-104
26	29	29.0	13	4	US-09-229-911A-102
27	29	29.0	13	4	US-09-229-911A-104

28	29	29.0	14	4	US-08-182-967-23	Sequence 23, Appl
29	29	29.0	15	1	US-07-689-693B-12	Sequence 12, Appl
30	29	29.0	15	3	US-09-230-222-3	Sequence 3, Appli
31	28.5	28.5	17	2	US-08-400-115-24	Sequence 24, Appl
32	28	28.0	9	3	US-09-258-754-63	Sequence 63, Appl
33	28	28.0	9	3	US-09-042-107-63	Sequence 63, Appl
34	28	28.0	9	4	US-09-722-250B-63	Sequence 11, Appl
35	28	28.0	10	5	PCT-US92-07865-11	Sequence 11, Appl
36	28	28.0	13	4	US-09-111-681C-5	Sequence 8, Appli
37	28	28.0	13	4	US-09-111-681C-8	Sequence 13, Appl
38	28	28.0	13	4	US-09-111-681C-13	Sequence 16, Appl
39	28	28.0	14	4	US-09-148-712-16	Sequence 16, Appl
40	28	28.0	15	4	US-09-947-372A-19	Sequence 19, Appl
41	28	28.0	17	1	US-08-141-892A-8	Sequence 8, Appli
42	28	28.0	17	1	US-08-141-892A-41	Sequence 41, Appl
43	28	28.0	17	2	US-08-583-447A-8	Sequence 8, Appli
44	28	28.0	17	2	US-08-583-447A-41	Sequence 41, Appl
45	28	28.0	17	2	US-08-583-447A-41	Sequence 41, Appl

## ALIGNMENTS

## RESULT 1

US-08-983-157B-22  
; Sequence 22, Application US/08983157B  
; Patent No. 6579848  
; GENERAL INFORMATION:  
; APPLICANT: HEARING, Vincent J., Jr.  
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal Protein and Peptides Thereof  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Needle & Rosenberg, P.C.  
; STREET: 127 Peachtree St., N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30303-1811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/983,157B  
; FILING DATE: 22-Dec-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/10695  
; FILING DATE: 21 JUN 1996  
; APPLICATION NUMBER: 60/ 000,436  
; FILING DATE: 23 JUN 1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spratt, Gwendolyn D.  
; REGISTRATION NUMBER: 36,016  
; REFERENCE/DOCKET NUMBER: 14014.0195  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-08-983-157B-22

Query Match 37.0%; Score 37; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 15;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

us-09-761-636a-8.closed.ra1

Sun Sep 5 11:41:19 2004

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QY      8 STNFKCKP 16
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Db      1 ATNDSCKP 9

RESULT 2
US-09-644-600-78
; Sequence 78, Application US/09644600
; Patent No. 6451500
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotochi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/644,600
; CURRENT FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: 09/027,337
; PRIOR FILING DATE: 1998-02-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 495-503 of the TADG-15 protein
US-09-644-600-78

Query Match      32.0%; Score 32; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 NTFCKP 15
      :||| |||||
Db      4 NKFCCKP 9

RESULT 3
US-09-654-600A-78
; Sequence 78, Application US/09654600A
; Patent No. 6649741
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Tanimoto, Hirotochi
; TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
; TITLE OF INVENTION: Overexpressed in Carcinomas
; FILE REFERENCE: D6064CIP/D
; CURRENT APPLICATION NUMBER: US/09/654,600A
; CURRENT FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/421,213
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 78
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Residues 495-503 of the TADG-15 protein
US-09-654-600A-78

Query Match      32.0%; Score 32; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      10 NTFCKP 15
      :||| |||||
Db      4 NKFCCKP 9

RESULT 4
US-08-053-079A-4
; Sequence 4, Application US/08053079A
; Patent No. 5606026
; GENERAL INFORMATION:
; APPLICANT: Rodman
; APPLICANT: Natural Human Igm Antibodies
; TITLE OF INVENTION: 15
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby
; STREET: 805 Third Ave.
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,079A
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Robinson, Joseph, R.
; REGISTRATION NUMBER: 33,448
; REFERENCE/DOCKET NUMBER: 4436/16060US4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)527-7700
; TELEFAX: (212)753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Human immunodeficiency virus type 1
; IMMEDIATE SOURCE:
; CLONE: tat #4
US-08-053-079A-4

Query Match      32.0%; Score 32; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      9 TNTFCCKPPC 17
      :||| :|||
Db      2 TNCYCKKCC 10

RESULT 5
US-08-685-589A-228
; Sequence 228, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

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STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/685,589A  
FILING DATE: 24-JUL-1996  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 8067-026-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-790-9090  
TELEFAX: 212-869-9741  
TELEX: 66141  
INFORMATION FOR SEQ ID NO: 228:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: circular  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..12  
OTHER INFORMATION: /product= "Cyclic"  
FEATURE:  
NAME/KEY: Modified-site  
LOCATION: 12  
OTHER INFORMATION: /product= "Xaa=Cha=cyclohexylalanine"  
US-08-685-589A-228

Query Match 32.0%; Score 32; DB 2; Length 12;  
Best Local Similarity 83.3%; Pred. No. 1e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 FCKPFC 17  
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DB 2 FCKPFC 7

RESULT 6  
US-09-462-118-4  
; Sequence 4, Application US/09462118  
; Patent No. 6610833  
; GENERAL INFORMATION:  
; APPLICANT: Rodman, Toby C.  
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies  
; FILE REFERENCE: 4436/1C074-US1  
; CURRENT APPLICATION NUMBER: US/09/462,118  
; CURRENT FILING DATE: 1999-12-18  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Human  
US-09-462-118-4

Query Match 32.0%; Score 32; DB 4; Length 12;  
Best Local Similarity 55.6%; Pred. No. 1e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 TMTCKPFC 17  
| | | |

Db 2 TNCYCKKC 10

RESULT 7  
US-08-369-566-1  
; Sequence 1, Application US/08369566  
; Patent No. 5650151  
; GENERAL INFORMATION:  
; APPLICANT: Bausher, Michael G  
; TITLE OF INVENTION: Citrus Proteins for Use in Field  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: USDA-ARS  
; STREET: Room 408, Bldg 005, BARC-W  
; CITY: Beltsville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20705  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/369,566  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/792,508  
; FILING DATE:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 301-344-1003  
; TELEFAX: 301-344-5060  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-369-566-1

Query Match 32.0%; Score 32; DB 1; Length 16;  
Best Local Similarity 54.5%; Pred. No. 1.4e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GKSTNTCKPP 16  
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DB 1 GEGTATFYTPP 11

RESULT 8  
US-08-983-157B-21  
; Sequence 21, Application US/08983157B  
; Patent No. 6579848  
; GENERAL INFORMATION:  
; APPLICANT: HEARING, Vincent J., Jr.  
; TITLE OF INVENTION: Depigmenting Activity of Agouti Signal  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Needle & Rosenberg, P.C.  
; STREET: 127 Peachtree St., N.E.  
; CITY: Atlanta  
; STATE: GA  
; COUNTRY: USA  
; ZIP: 30303-1811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30

us-09-761-636a-8.closed.ra1

Sun Sep 5 11:41:19 2004

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,157B
; FILING DATE: 22-Dec-1997
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10695
; FILING DATE: 21 JUN 1996
; APPLICATION NUMBER: 60/ 000,436
; FILING DATE: 23 JUN 1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Szatt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 14014.0195
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
;
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-983-157B-21

Query Match      31.0%; Score 31; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      8 STWTFCKPP 16
DB      1 ATRDSCKPP 9

RESULT 9
US-09-328-501-4
; Sequence 4, Application US/09328501A
; Patent No. 6258581
; GENERAL INFORMATION:
; APPLICANT: ITO, Makoto
; TITLE OF INVENTION: Ceramidase Gene
; FILE REFERENCE: 1422-0377P
; CURRENT APPLICATION NUMBER: US/09/328,501A
; CURRENT FILING DATE: 1999-06-09
; EARLIER APPLICATION NUMBER: 10-234769 JAPAN
; EARLIER FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; OTHER INFORMATION: any n or Xaa = Unknown
US-09-328-501-4

Query Match      31.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 SELGKSTNWF 12
DB      2 SEIGGSTRSF 11

RESULT 10
US-09-777-710A-4
; Sequence 4, Application US/09777710A
; Patent No. 6489117
; GENERAL INFORMATION:
; APPLICANT: OKINO, No. 6489117omu et al.
;
; TITLE OF INVENTION: CERAMIDASE GENE
; FILE REFERENCE: 1422-0458P
; CURRENT APPLICATION NUMBER: US/09/777,710A
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-777-710A-4

Query Match      31.0%; Score 31; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      3 SELGKSTNWF 12
DB      2 SEIGGSTRSF 11

RESULT 11
US-08-882-046-9
; Sequence 9, Application US/08882046
; Patent No. 6136952
; GENERAL INFORMATION:
; APPLICANT: Li, Linheng
; APPLICANT: Hood, Leroy
; APPLICANT: Krantz, Ian D. B.
; TITLE OF INVENTION: Human Jagged Polypeptide, Encoding
; TITLE OF INVENTION: Nucleic Acids and Methods of Use
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,046
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-UW 2637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-882-046-9

Query Match      31.0%; Score 31; DB 3; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      6 GKSTNTFCCKP 15
DB      7 GFGCNKCRCRP 16

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## RESULT 12

US-09-252-586-19  
 ; Sequence 19, Application US/09252586  
 ; Patent No. 6387643  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heintrikson, Robert L.  
 ; APPLICANT: Fairbanks, Michael B.  
 ; APPLICANT: Milner, Ana M.  
 ; TITLE OF INVENTION: Human Platelet Heparanase Polypeptides,  
 ; TITLE OF INVENTION: Polynucleotide Heparanase That Encode Them, and Methods For  
 ; TITLE OF INVENTION: the Identification of Compounds That Alter Heparanase  
 ; NUMBER OF SEQUENCES: 29  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pharmacia & Upjohn  
 ; STREET: 301 Henrietta  
 ; CITY: Kalamazoo  
 ; STATE: MI  
 ; COUNTRY: USA  
 ; ZIP: 49001  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: PC-DOS/MS-DOS  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/252,586  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kerber, Lori L.  
 ; REGISTRATION NUMBER: 41,113  
 ; REFERENCE/DOCKET NUMBER: 6131.N CN1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 616-833-0974  
 ; TELEFAX: 616-833-8897  
 ; INFORMATION FOR SEQ ID NO: 19:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 17 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; US-09-252-586-19

Query Match 31.0%; Score 31; DB 4; Length 17;  
 Best Local Similarity 54.5%; Pred. No. 2.1e+02;  
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 ELGKSTNTPCK 14  
 ||| |  
 Db 7 ELGNEPNSFLK 17

## RESULT 13

US-08-443-965B-9  
 ; Sequence 9, Application US/08443965B  
 ; Patent No. 5821341  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McClelland, Alan  
 ; APPLICANT: Greve, Jeffrey M.  
 ; TITLE OF INVENTION: Soluble Molecule Related to but  
 ; TITLE OF INVENTION: Distinct from ICAM-1  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bayer Corporation  
 ; STREET: 400 Morgan Lane  
 ; CITY: West Haven  
 ; STATE: Connecticut  
 ; COUNTRY: USA  
 ; ZIP: 06516  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" diskette, 1.44 MB storage

; COMPUTER: IBM Thinkpad 760ED  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: WordPerfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/443,965B  
 ; FILING DATE: 18-MAY-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/425,989  
 ; FILING DATE: 20-APR-1995  
 ; APPLICATION NUMBER: 08/156,653  
 ; FILING DATE: 22-NOV-1993  
 ; APPLICATION NUMBER: 08/005,204  
 ; FILING DATE: 15-JAN-1993  
 ; APPLICATION NUMBER: 07/449,356  
 ; FILING DATE: 21-DEC-1989  
 ; APPLICATION NUMBER: 07/445,951  
 ; FILING DATE: 13-DEC-1989  
 ; APPLICATION NUMBER: 07/301,192  
 ; FILING DATE: 24-JAN-1989  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Barbara A. Shimei  
 ; REGISTRATION NUMBER: 29,862  
 ; REFERENCE/DOCKET NUMBER: MTI 209.2C3D2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (203) 812-2786  
 ; TELEFAX: (203) 812-5492  
 ; INFORMATION FOR SEQ ID NO: 9:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 14 amino acid residues  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: no  
 ; FRAGMENT TYPE: C-terminal fragment  
 ; FEATURE:  
 ; NAME/KEY: modified ICAM fragment  
 ; LOCATION: C-terminus  
 ; OTHER INFORMATION: first 11 amino acid  
 ; OTHER INFORMATION: residues correspond to the C-terminus of  
 ; OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate  
 ; OTHER INFORMATION: coupling  
 ; US-08-443-965B-9

Query Match 30.0%; Score 30; DB 2; Length 14;  
 Best Local Similarity 62.5%; Pred. No. 2.4e+02;  
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NTFCKPCC 17  
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 Db 7 NTQATPPC 14

## RESULT 14

US-08-425-989B-9  
 ; Sequence 9, Application US/08425989B  
 ; Patent No. 5849699  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McClelland, Alan  
 ; APPLICANT: Greve, Jeffrey M.  
 ; TITLE OF INVENTION: Soluble Molecule Related to but  
 ; TITLE OF INVENTION: Distinct from ICAM-1  
 ; NUMBER OF SEQUENCES: 13  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Bayer Corporation  
 ; STREET: 400 Morgan Lane  
 ; CITY: West Haven  
 ; STATE: Connecticut  
 ; COUNTRY: USA  
 ; ZIP: 06516  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" diskette, 1.44 MB storage  
 ; COMPUTER: IBM Thinkpad 760ED

us-09-761-636a-8.closed.ra1

Sun Sep 5 11:41:19 2004

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; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,989B
; FILING DATE: 20-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/156,653
; FILING DATE: 22-NOV-1993
; APPLICATION NUMBER: 08/005,204
; FILING DATE: 15-JAN-1993
; APPLICATION NUMBER: 07/449,356
; FILING DATE: 21-DEC-1989
; APPLICATION NUMBER: 07/445,951
; FILING DATE: 13-DEC-1989
; APPLICATION NUMBER: 07/301,192
; FILING DATE: 24-JAN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara A. Shimei
; REGISTRATION NUMBER: 29,862
; REFERENCE/DOCKET NUMBER: MTI 209.2C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2786
; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acid residues
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; HYPOTHETICAL: no
; FRAGMENT TYPE: C-terminal fragment
; FEATURE:
; NAME/KEY: modified ICAM fragment
; LOCATION: C-terminus
; OTHER INFORMATION: first 11 amino acid
; OTHER INFORMATION: residues correspond to the C-terminus of
; OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate
; OTHER INFORMATION: coupling
; US-08-425-989B-9

Query Match 30.0%; Score 30; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NTFCKPPC 17
Db 7 NTQATPPC 14

US-08-443-966B-9

APPLICATION NUMBER: US/08/443,966B
FILING DATE: 18-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/425,989
FILING DATE: 20-APR-1995
APPLICATION NUMBER: 08/156,653
FILING DATE: 22-NOV-1993
APPLICATION NUMBER: 08/005,204
FILING DATE: 15-JAN-1993
APPLICATION NUMBER: 07/449,356
FILING DATE: 21-DEC-1989
APPLICATION NUMBER: 07/445,951
FILING DATE: 13-DEC-1989
APPLICATION NUMBER: 07/301,192
FILING DATE: 24-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Barbara A. Shimei
REGISTRATION NUMBER: 29,862
REFERENCE/DOCKET NUMBER: MTI 209.2C3D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2786
TELEFAX: (203) 812-5492
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: C-terminal fragment
FEATURE:
NAME/KEY: modified ICAM fragment
LOCATION: C-terminus
OTHER INFORMATION: first 11 amino acid
OTHER INFORMATION: residues correspond to the C-terminus of
OTHER INFORMATION: ICAM; last residue (Cys) added to facilitate
OTHER INFORMATION: coupling
US-08-443-966B-9

Query Match 30.0%; Score 30; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 NTFCKPPC 17
Db 7 NTQATPPC 14

Search completed: September 5, 2004, 10:56:57
Job time : 21 secs

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RESULT 15
US-08-443-966B-9
; Sequence 9, Application US/08443966B
; Patent No. 5859212
; GENERAL INFORMATION:
; APPLICANT: McClelland, Alan
; APPLICANT: Greve, Jeffrey M.
; TITLE OF INVENTION: Soluble Molecule Related to but
; TITLE OF INVENTION: Distinct from ICAM-1
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 MB storage
; COMPUTER: IBM ThinkPad 760ED
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6567 Seconds  
(without alignments)  
74.205 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	24	43.6	9	2	C24180		fibrinogen beta ch
2	19	34.5	8	2	PC1002		leucine-tRNA ligas
3	18	32.7	6	4	I79564		hypothetical TCU3
4	18	32.7	9	2	D24180		fibrinogen beta ch
5	18	32.7	9	2	PH0942		T-cell receptor be
6	17	30.9	6	2	S29637		jacalin beta-II ch
7	17	30.9	6	2	I37263		Y protein - human
8	17	30.9	7	2	PH0932		T-cell receptor be
9	17	30.9	9	2	D28854		fibrinopeptide B -
10	17	30.9	9	2	E28854		fibrinopeptide B -
11	17	30.9	9	2	F28854		fibrinopeptide B -
12	16	29.1	9	2	PH0935		T-cell receptor be
13	16	29.1	9	2	PH0921		T-cell receptor be
14	15	27.3	6	2	JU0355		lipopeptide WS1279
15	15	27.3	7	2	B39040		calsequestrin, fas
16	15	27.3	8	2	S59622		metallothionein is
17	15	27.3	8	2	S19288		acylase - Kluyvera
18	15	27.3	8	2	S69165		ferredoxin a2 - Ja
19	15	27.3	9	2	A11497		transaldolase (EC
20	15	27.3	9	2	A26363		cardioactive pepti
21	15	27.3	9	2	S27233		cardioactive pepti
22	15	27.3	9	2	PH0917		cardioactive pepti
23	15	27.3	9	2	S39767		T-cell receptor be
24	14	25.5	6	2	B31263		cardioactive pepti
25	14	25.5	6	2	S29881		dihydrofolate redu
26	14	25.5	7	1	KEYDGD		Na+/K+-exchanging
27	14	25.5	8	2	B47594		galactose oxidase
28	14	25.5	8	2	A61230		aspartate kinase
29	14	25.5	9	2	B39504		calsequestrin, car
							octamer-binding pr

## ALIGNMENTS

### RESULT 1

C24180  
fibrinogen beta chain - Japanese macaque (fragment)  
N:Contains: fibrinopeptide B

C:Species: Macaca fuscata (Japanese macaque)

C>Date: 05-Jun-1988 #sequence\_revision 10-Mar-1994 #text\_change 26-Jan-1996  
C/Accession: C24180

R:Nakamura, S.; Takenaka, O.; Takahashi, K.

A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E

uenons, and baboons.

A/Reference number: A91990; MUID:85289140; PMID:3928610

A/Accession: C24180

A/Molecule type: protein

A/Residues: 1-9 <NAK>

C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 43.6%; Score 24; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEESL 7

Db 1 NEESL 5

### RESULT 2

PC1002  
leucine-tRNA ligase (EC 6.1.1.4) - Escherichia coli (fragments)  
N/Alternate names: leucyl-tRNA synthetase

C/Species: Escherichia coli

C>Date: 17-Aug-1992 #sequence\_revision 17-Aug-1992 #text\_change 03-Jun-2002  
C/Accession: PC1002

R:Miao, F.; Shi, J.P.; Wang, Y.L.

A/Title: Chemical modification of sulfhydryl groups of E. coli leucyl-tRNA synthetase an

A/Reference number: PC1002

A/Accession: PC1002

A/Molecule type: protein

A/Residues: 1-8 <MIA>

C/Comment: This enzyme catalyzes the aminoacylation of tRNA(Leu) with Leucine.  
C/Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

F;5-8/Region: catalytic #status predicted

Query Match 34.5%; Score 19; DB 2; Length 8;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCN 3

Db 4 CCD 6

Sun Sep 5 11:41:22 2004

```
RESULT 3
I79564
hypothetical TCl3 protein (mistranslated) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C:Accession: I79564
R:Zurter, M.; Hockett, R.D.; Roberts, C.W.; McGuire, E.A.; Bloomstone, J.; Morton, C.C.;
Proc. Natl. Acad. Sci. U.S.A. 87, 3161-3165, 1990
A:Title: The t(10;14)(q24;q11) of T-cell acute lymphoblastic leukemia juxtaposes the del
A:Reference number: 159162; MUID:90222189; PMID:2326274
C:Accession: I79564
A:Accession: not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <ZUT>
A:CROSS-references: GB:M33602; NID:g3339907; PIDN:AAA66449.1; PID:g807656
C:Comment: This is the hypothetical translation of a sequence translated in an incorrect
Query Match 32.7%; Score 18; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CC 2
Db 3 CC 4
RESULT 4
D24180
fibrinogen beta chain - red guenon (fragment)
N:Contains: fibrinopeptide B
C:Species: Erythrocybus patas (red guenon, hussar)
C>Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C:Accession: D24180
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A:Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (B
A:Reference number: A91990; MUID:85289140; PMID:3928610
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 NEESL 7
Db 1 NEEVL 5
RESULT 5
PH0342
T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0342
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergi
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0942
A:Molecule type: mRNA
A:Residues: 1-9 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon TGC for residue 2 as Ala
C:Keywords: T-cell receptor
Query Match 32.7%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CC 2
Db 3 CC 4
RESULT 6
S29637
Jacalin beta-II chain - Artocarpus champeden (fragment)
C:Species: Artocarpus champeden
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S29637
R:Ngoc, L.D.; Brillard, M.; Hoebeke, J.
Biochim. Biophys. Acta 1156, 219-222, 1993
A:Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD
A:Reference number: S29635; MUID:93152601; PMID:8427879
C:Accession: S29637
A:Molecule type: protein
A:Residues: 1-6 <NGO>
A:Experimental source: seed
A:Complex: heterotetramer; two alpha and two beta chains
C:Function:
A:Description: seed storage protein
A>Note: lectin for D-galactosyl-beta-1->3-N-acetylgalactosamine
C:Keywords: heterotetramer; lectin; seed; storage protein
Query Match 30.9%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 NEES 6
Db 1 NEQS 4
RESULT 7
I37263
Y protein - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 05-Nov-1999
C:Accession: I37263
R:Waeber, G.; Habener, J.F.
Endocrinology 131, 2010-2015, 1992
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an altern
A:Reference number: I37263; MUID:93010691; PMID:1396344
C:Accession: I37263
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6 <RES>
A:CROSS-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C:Genetics:
A:Gene: CREB
Query Match 30.9%; Score 17; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 6 SLIC 9
Db 1 SLFC 4
RESULT 8
PH0932
T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0932
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0932
```

A:Molecule type: mRNA  
 A:Residues: 1-7 <GOL>  
 A:Experimental source: complete Freund's adjuvant-immunized lymph node  
 C:Keywords: T-cell receptor

Query Match 30.9%; Score 17; DB 2; Length 7;  
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCNEESL 7  
 | : |  
 Db 1 CASPERL 7

## RESULT 9

F28854  
 fibrinopeptide B - olive baboon  
 C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)  
 C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Aug-2000  
 C:Accession: D28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. 94, 1973-1978, 1983  
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)  
 A:Reference number: A91973; MUID:84161822; PMID:6423621  
 A:Accession: D28854

A:Molecule type: protein  
 A:Residues: 1-9 <NAK>  
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7  
 | : |  
 Db 1 NOEGL 5

## RESULT 10

E28854  
 fibrinopeptide B - hamadryas baboon  
 C:Species: Papio hamadryas (hamadryas baboon)  
 C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Aug-2000  
 C:Accession: E28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. 94, 1973-1978, 1983  
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)  
 A:Reference number: A91973; MUID:84161822; PMID:6423621  
 A:Accession: E28854

A:Molecule type: protein  
 A:Residues: 1-9 <NAK>  
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7  
 | : |  
 Db 1 NOEGL 5

## RESULT 11

F28854  
 fibrinopeptide B - gelada baboon  
 C:Species: Theropithecus gelada (gelada baboon)  
 C:Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Aug-2000  
 C:Accession: F28854

R:Nakamura, S.; Takenaka, O.; Takahashi, K.  
 J. Biochem. 94, 1973-1978, 1983  
 A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)  
 A:Reference number: A91973; MUID:84161822; PMID:6423621  
 A:Accession: F28854

A:Molecule type: protein  
 A:Residues: 1-9 <NAK>  
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 30.9%; Score 17; DB 2; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7  
 | : |  
 Db 1 NOEGL 5

## RESULT 12

PH0935  
 T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C:Accession: PH0935

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic arthritis  
 A:Reference number: PH0891; MUID:92078857; PMID:1836012  
 A:Accession: PH0935

A:Molecule type: mRNA  
 A:Residues: 1-9 <GOL>  
 A:Experimental source: complete Freund's adjuvant-immunized lymph node  
 C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6  
 | : |  
 Db 1 CASSET 6

## RESULT 13

PH0921  
 T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C:Accession: PH0921

R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic arthritis  
 A:Reference number: PH0891; MUID:92078857; PMID:1836012  
 A:Accession: PH0921

A:Molecule type: mRNA  
 A:Residues: 1-9 <GOL>  
 A:Experimental source: concanavalin A-activated lymphoblast  
 C:Keywords: T-cell receptor

Query Match 29.1%; Score 16; DB 2; Length 9;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6  
 | : |  
 Db 1 CASSEN 6

## RESULT 14

JU0355  
 lipopeptide WS1279 [validated] - Streptomyces willmorei  
 C:Species: Streptomyces willmorei  
 C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: JU0355

R:Tsuda, Y.; Okada, Y.; Tanaka, M.; Shigematsu, N.; Hori, Y.; Goto, T.; Hashimoto, M.  
 Chem. Pharm. Bull. 39, 607-611, 1991  
 A:Title: Structure and synthesis of an immunoreactive lipopeptide, WS1279, of microbial origin  
 A:Reference number: JU0355; MUID:91300586; PMID:2070441

A;Accession: JU0355  
A;Molecule type: protein  
A;Residues: 1-6 <FSU>  
A;Note: the structure was confirmed by synthesis  
C;Keywords: blocked amino end; lipoprotein  
F;Binding site: sn-2,3-diacylglycerol (Cys) (covalent) #status experimental  
F;Modified site: fatty acylated amino end (Cys) #status experimental

Query Match 27.3%; Score 15; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CN 3  
|||  
DB 1 CN 2

RESULT 15  
B39040  
C;Species: Oryctolagus cuniculus (domestic rabbit)  
C;Date: 23-Aug-1991 #sequence\_revision 23-Aug-1991 #text\_change 23-Feb-1997  
C;Accession: B39040  
R;Cala, S.E.; Jones, L.R.  
J. Biol. Chem. 266, 391-398, 1991  
A;Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by casein  
A;Reference number: A39040; MUID:91093153; PMID:1985907  
A;Accession: B39040  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <CAL>  
C;Keywords: phosphoprotein; skeletal muscle

Query Match 27.3%; Score 15; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEESL 7  
:|:  
DB 2 DEEDL 6



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:57:02 ; Search time 7 Seconds  
(without alignments)  
66.947 Million cell updates/sec

Title: US-09-761-636A-9  
Perfect score: 55  
Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues  
Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	43.6	9	1	FIBB MACFU
2	18	32.7	9	1	FIBB ERYPA
3	17	30.9	9	1	FIBB PAPAN
4	17	30.9	9	1	FIBB PAPA
5	17	30.9	9	1	FIBB THEGE
6	16	29.1	9	1	ULAK MOUSE
7	15	27.3	9	1	CCAP CARMA
8	15	27.3	9	1	TAL3 PICJA
9	14	25.5	7	1	IGAO DACDE
10	13	23.6	5	1	TRM3 ECOLI
11	13	23.6	8	1	PLP BRANA
12	13	23.6	9	1	SAME MUSCA
13	12	21.8	7	1	UF03 MOUSE
14	12	21.8	8	1	UPA1 HUMAN
15	12	21.8	9	1	SAP STOVA
16	12	21.8	9	1	TALI PICJA
17	11	20.0	7	1	BRHP CONIM
18	11	20.0	7	1	FARI ASCSU
19	11	20.0	8	1	CADI ENTFA
20	11	20.0	9	1	TR33 BOVIN
21	11	20.0	9	1	UPA7 HUMAN
22	10	18.2	8	1	ACT CARMA
23	10	18.2	9	1	FAR4 CALVO
24	10	18.2	9	1	OXYT BUFRE
25	9	16.4	6	1	TMOF SARBU
26	9	16.4	8	1	COW2 CONPU
27	9	16.4	8	1	GLUR HUMAN
28	9	16.4	9	1	CONO CONGE
29	9	16.4	9	1	CONO CONST
30	9	16.4	9	1	COW CONVE
31	9	16.4	9	1	DNFI LOOMI
32	9	16.4	9	1	ISOT CYPCA
33	9	16.4	9	1	MGMT_BOVIN

34	9	16.4	9	1	OXYA SCYCA	P42996 scyllorhinu
35	9	16.4	9	1	OXYA SQAC	P42999 squalus aca
36	9	16.4	9	1	OXYF SCYCA	P42997 scyllorhinu
37	9	16.4	9	1	OXYT CYPCA	P23879 cyprinus ca
38	9	16.4	9	1	OXYT EISFO	P42998 eisenia foe
39	9	16.4	9	1	OXYT OCTVU	P80027 octopus vul
40	9	16.4	9	1	OXYT RABIT	P32878 oryctolagus
41	9	16.4	9	1	OXYT RAUCL	P42994 raja clavav
42	9	16.4	9	1	OXYV SQAC	P43000 squalus aca
43	9	16.4	9	1	UF02 MOUSE	P38640 mus musculu
44	9	16.4	9	1	UN19 CLOPA	P81355 clostridium
45	8	14.5	6	1	ACPH_RABIT	P25154 oryctolagus

## ALIGNMENTS

RESULT 1  
FIBB MACFU STANDARD; PRT; 9 AA.  
AC P19345;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).  
GN FGB.  
OS Macaca fuscata fuscata (Japanese macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;  
OC Cercopitheidae; Macaca.  
OX NCBI\_TaxID=9543;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=85289140; PubMed=3928610;  
RA Nakamura S., Takenaka O., Takahashi K.;  
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and  
RT patas monkey (Erythrocebus patas): their amino acid sequences,  
RT restricted mutations, and a molecular phylogeny for macaques,  
RT guenons, and baboons.";  
RL J. Biochem. 97:1487-1492(1985).  
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that  
CC polymerize into fibrin and acting as a cofactor in platelet  
CC aggregation.  
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
CC which cleaves fibrinopeptides A and B from alpha and beta chains,  
CC and thus exposes the N-terminal polymerization sites responsible  
CC for the formation of the soft clot.  
DR PIR; C24180; C24180.  
DR InterPro; IPR002181; Fibrinogen C.  
DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
KW Blood coagulation; Plasma.  
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
FT NON TER 9 9  
SQ SEQUENCE 9 AA; 1038 MW; 69FE65B9C735BB1B CRC64;

Query Match 43.6%; Score 24; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEESL 7  
Db 1 NEESL 5

RESULT 2  
FIBB ERYPA STANDARD; PRT; 9 AA.  
AC P19346;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Erythrocybus patas (Red guenon) (Hussar).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Erythrocebus.
OX NCBI_TaxID=9538;
RN [1]
RP SEQUENCE.
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492 (1985).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; D24180;
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1020 MW; 69FE7879C732CB1B CRC64;

Query Match 32.7%; Score 18; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NEEVL 5

RESULT 3
FIBB PAPAN
ID FIBB PAPAN STANDARD; PRT; 9 AA.
AC P19344;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; D24180;
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71B9C7287B06 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NQEGL 5

RESULT 5
FIBB THEGE
ID FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

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DR PIR; D28854; D28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1076 MW; DDFE6409C7287B06 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NQEGL 5

RESULT 4
FIBB PAPA
ID FIBB PAPA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978 (1983).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; E28854; E28854.
DR InterPro; IPR002181; Fibrinogen C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDFE71B9C7287B06 CRC64;

Query Match 30.9%; Score 17; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NEESL 7
Db 1 NQEGL 5

RESULT 5
FIBB THEGE
ID FIBB THEGE STANDARD; PRT; 9 AA.
AC P19342;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

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GN FGB.  
 OS Theropithecus gelada (Gelada baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Theropithecus.  
 OX NCBI\_TaxID=9565;  
 RN [1]  
 RN SEQUENCE.  
 RX MEDLINE=84161822; PubMed=6423621;  
 RA Nakamura S., Takenaka O., Takahashi K.;  
 RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,  
 RT and Theropithecus gelada): their amino acid sequences and  
 RT evolutionary rates and a molecular phylogeny for the baboons.";  
 RL J. Biochem. 94:1973-1978 (1983).  
 CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that  
 CC polymerize into fibrin and acting as a cofactor in platelet  
 CC aggregation.  
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS  
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.  
 CC -!- PFM: Conversion of fibrinogen to fibrin is triggered by thrombin,  
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,  
 CC and thus exposes the N-terminal polymerization sites responsible  
 CC for the formation of the soft clot.  
 DR PIR; F28854; F28854.  
 DR InterPro; IPR002181; Fibrinogen.C.  
 DR PROSITE; PS00514; FIBRIN\_AG\_C\_DOMAIN; PARTIAL.  
 KW Blood coagulation; Plasma.  
 FT PEPTIDE 1 9 FIBRINOPEPTIDE B.  
 FT NON TER 9 9  
 SQ SEQUENCE 9 AA; 977 MW; DDFE7879C7287B06 CRC64;  
 Query Match 30.9%; Score 17; DB 1; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 NEESL 7  
 | : | |  
 Db 1 NOEGL 5

RESULT 6  
 ULAK\_MOUSE  
 ID ULAK\_MOUSE STANDARD; PRT; 9 AA.  
 AC P99031;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)  
 DE (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE.  
 RP TISSUE=Liver;  
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,  
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,  
 RA Cowthorne M.;  
 RL Submitted (AUG-1998) to Swiss-Prot.  
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
 CC protein is: 6.0, its MW is: 12.5 kDa.  
 CC SWISS-2DPAGE; P99031; MOUSE.  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1106 MW; E1B842C3240B145A CRC64;

Query Match 29.1%; Score 16; DB 1; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 3 NEESL 8  
 | : |  
 Db 3 NERKVI 8

RESULT 7  
 CCAP\_CARMA  
 ID CCAP\_CARMA STANDARD; PRT; 9 AA.  
 AC P38556;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Cardioactive peptide (CCAP).  
 OS Carcinus maenas (Common shore crab) (Green crab),  
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),  
 OS Tenebrio molitor (Yellow mealworm), and  
 OS Spodoptera eridania (Southern armyworm).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunodea; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759, 7130, 7067, 37547;  
 RN [1]  
 RN SEQUENCE.  
 RP SPECIES=C.maenas; TISSUE=Pericardial organs;  
 RC Stangier J., Hilbich C., Beyreuther K., Keller R.;  
 RA "Unusual cardioactive peptide (CCAP) from pericardial organs of the  
 RT shore crab Carcinus maenas.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).  
 RN [2]  
 RN SEQUENCE.  
 RP SPECIES=M.sexta;  
 RC MEDLINE=93050243; PubMed=1426284;  
 RX Cheung C.-C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;  
 RA "Primary structure of a cardioactive neuropeptide from the tobacco  
 RT hawkmoth, Manduca sexta.";  
 RL FEBS Lett. 313:165-168 (1992).  
 RN [3]  
 RN SEQUENCE.  
 RP SPECIES=T.molitor, and S.eridania; TISSUE=Head;  
 RC MEDLINE=94176032; PubMed=8129851;  
 RX Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,  
 RA Schooley D.A.;  
 RT "Isolation and identification of a cardioactive peptide from Tenebrio  
 RL molitor and Spodoptera eridania.";  
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).  
 CC -!- FUNCTION: The effect of CCAP is both ino- and chronotropic.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Stored in pericardial organs and released  
 CC into the hemolymph.  
 DR PIR; A26363; A26363.  
 DR PIR; S27233; S27233.  
 KW Neuropeptide; Amidation.  
 FT DISULFID 3 9  
 FT MOD RES 9 9 AMIDATION.  
 SQ SEQUENCE 9 AA; 959 MW; CSA861A9CDD44EB9 CRC64;  
 Query Match 27.3%; Score 15; DB 1; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 CN 3  
 | |  
 Db 3 CN 4

RESULT 8  
 TAL3\_PICUA  
 ID TAL3\_PICUA STANDARD; PRT; 9 AA.  
 AC P17441;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Transaldolase III (EC 2.2.1.2) (Fragment).  
 OS Pichia jadinii (Yeast) (Candida utilis).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Pichia.

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OX NCBI_TaxID=4903;
RN [1]
RP SEQUENCE.
RX MEDLINE=75145197; PubMed=1092268;
RA Tsolas O., Sun S.C.;
RT "Isolation of a peptide containing a histidyl-cysteiny sequence
RT from the active center of transaldolase.";
RL Arch. Biochem. Biophys. 167:525-533(1975).
CC -!- FUNCTION: Transaldolase is important for the balance of
CC metabolites in the pentose-phosphate pathway.
CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
CC 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
CC -!- SIMILARITY: Belongs to the transaldolase family. Subfamily 1.
DR PIR; A11497; A11497.
DR InterPro; IPR001585; Transaldolase.
DR PROSITE; PS00958; TRANSALDOLASE_2; PARTIAL.
DR PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
KW Transferase; Pentose shunt.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1033 MW; 325A31A44EB1E058 CRC64;

Query Match 27.3%; Score 15; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CN 3
Db |||
5 CN 6

RESULT 9
IGAO DACDE
ID IGAC DACDE STANDARD; PRT; 7 AA.
AC P06294;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroides (Cladobotryum dendroides).
OC Eukaryota; Fungi; Ascomycota; Peizizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.
OX NCBI_TaxID=5132;
RN [1]
RP SEQUENCE.
RA Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
RT Dactylium dendroides.";
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: Binds one copper ion per molecule but does not bind the
CC galactose oxidase apoenzyme. It may inactivate the enzyme by
CC binding to its prosthetic copper group.
DR PIR; A01341; XEYDGD.
KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 25.5%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NEES 6
Db |||
4 NTES 7

RESULT 10
TRM3_ECOLI
ID TRM3_ECOLI STANDARD; PRT; 5 AA.
AC P13973;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DE Tram protein (Fragment).
GN TRAM.
OS Escherichia coli.
OG Plasmid IncFII R100.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88227859; PubMed=2836369;
RA Inamoto S., Yoshioka Y., Ohtsubo E.;
RT "Identification and characterization of the products from the traJ
RT and traY genes of plasmid R100.";
RL J. Bacteriol. 170:2749-2757(1988).
CC -!- FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION
CC PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the traM family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M20941; -; NOT_ANNOTATED_CDS.
DR PIR; A32014; A32014.
KW Conjugation; Plasmid; DNA-binding.
FT NON_TER 1
SQ SEQUENCE 5 AA; 634 MW; 6B1B1AA443500000 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEE 5
Db |||
2 NDE 4

RESULT 11
PLP_BRANA
ID PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DB Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RX STRAIN=CV. TOPAZ; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
FT NON_TER 8
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 NEE 5  
Db 5 NDE 7

RESULT 12  
SAMP MUSCA STANDARD; PRT; 9 AA.  
AC P19095;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Serum amyloid P-component (SAP) (Fragment).  
OS Musculus canis (Smooth dogfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;  
OC Blasombranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;  
OC Mustelus.  
OX NCBI\_TaxID=7812;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83160932; PubMed=6403520;  
RA Robey F.A., Tanaka T., Liu T.-Y.;  
RT "Isolation and characterization of two major serum proteins from the  
dogfish, Mustelus canis, C-reactive protein and amyloid P  
component.";  
RL J. Biol. Chem. 258:3889-3894 (1983).  
CC -I- SUBUNIT: Homopentamer. Pentaxin (or pentraxin) have a discoid  
arrangement of 5 noncovalently bound subunits.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND  
IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.  
CC -I- SIMILARITY: Belongs to the pentaxin family.  
DR PIR; B20569; B20569.  
DR InterPro; IPR001759; Pentaxin.  
DR PROSITE; PS00289; PENTAXIN; PARTIAL.  
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.  
FT DOMAIN 1 >9 PENTAXIN.  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 23.6%; Score 13; DB 1; Length 9;  
Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 ESLI 8  
Db 5 KSLI 8

RESULT 13  
UF03 MOUSE STANDARD; PRT; 7 AA.  
AC P38641;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of fibroblasts (P36) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX TISSUE=Fibroblast; PubMed=75231108;  
RC MEDLINE=95009907; Wichter L.L., He C., Selkirk J.K.;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins  
using preparative two-dimensional gel electrophoresis.";  
RL Electrophoresis 15:735-745 (1994).  
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 5.1, its MW is: 36 kDa.  
FT NON\_TER 7 7

SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DB1B1180 CRC64;

Query Match 21.8%; Score 12; DB 1; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEE 6  
Db 1 HEEA 4

RESULT 14  
UPA1 HUMAN STANDARD; PRT; 8 AA.  
ID UPAL HUMAN  
AC P30067;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RX MEDLINE=93092937; PubMed=1459097;  
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,  
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,  
RA Hochrassner D.F.;  
RT "Plasma protein map: an update by microsequencing.";  
RL Electrophoresis 13:707-714 (1992).  
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
protein is: 4.9, its MW is: 65 kDa.  
DR SWISS-2DPAGE; P30067; HUMAN.  
FT NON\_TER 1 1  
FT UNSURE 8 8  
FT NON\_TER 8 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 21.8%; Score 12; DB 1; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.4e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NEE 6  
Db 1 DQES 4

RESULT 15  
SAP STOVA STANDARD; PRT; 9 AA.  
ID SAP STOVA  
AC P24047;  
DT 01-MAR-1992 (Rel. 21, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Sperm-activating peptide (SAP).  
OS Stomopneustes variolaris (Sea urchin).  
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
OC Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;  
OC Stomopneustes.  
OX NCBI\_TaxID=7663;  
RN [1]  
RP SEQUENCE, AND DISULFIDE BOND.  
RC TISSUE=Egg Jelly;  
RX MEDLINE=92097763; PubMed=1756858;  
RA Yoshino K.-I., Takao T., Shimonishi Y., Suzuki N.;  
RT "Determination of the amino acid sequence of an intramolecular  
disulfide linkage-containing sperm-activating peptide by tandem mass  
spectrometry.";  
RL Electrophoresis 15:735-745 (1994).  
CC -I- FUNCTION: Cause stimulation of sperm respiration and motility  
through intracellular alkalinization, transient elevations of

CC CAMP, cGMP and calcium levels in sperm cells, and transient  
CC activation and subsequent inactivation of the membrane form of  
CC guanylate cyclase.

FT DISULFID 3

SQ SEQUENCE 9 AA; 1010 MW; C469B3387B076EB9 CRC64;

Query Match

Best Local Similarity 21.8%; Score 12; DB 1; Length 9;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CNE 4

Db 3 CPE 5

Search completed: September 5, 2004, 11:04:00

Job time : 7 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:59:47 ; Search time 31.6667 Seconds  
(without alignments)  
89.674 Million cell updates/sec

Title: US-09-761-636A-9

Perfect score: 55

Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 840

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	32.7	8	Q8IV87	Q8IV87 homo sapien
2	18	32.7	8	Q9SAY7	Q9SAY7 dioscorea t
3	18	32.7	9	Q9FSZ2	Q9FSZ2 cicor ariet
4	18	32.7	9	Q8CG13	Q8CG13 mus musculus
5	18	32.7	9	Q9EIU7	Q9EIU7 hepatitis b
6	17	30.9	9	Q86SF0	Q86SF0 homo sapien
7	16	29.1	7	Q67113	Q67113 influenzavi
8	16	29.1	7	Q42564	Q42564 fugu rubrip
9	15	27.3	9	P82440	P82440 nicotiana t
10	15	27.3	9	O12096	O12096 caprine art
11	15	27.3	9	O12100	O12100 caprine art
12	15	27.3	9	O12102	O12102 caprine art
13	15	27.3	9	O12098	O12098 caprine art
14	15	27.3	9	O12104	O12104 caprine art
15	14	25.5	9	Q8MJT7	Q8MJT7 eulemur ful
16	14	25.5	9	Q8MJT8	Q8MJT8 eulemur ful

17	23.6	7	11	O55184	O55184 rattus norv
18	23.6	8	2	O32560	O32560 escherichia
19	23.6	8	11	P70243	P70243 mus musculu
20	23.6	9	6	Q9TUY0	Q9TUY0 monodelphis
21	23.6	9	11	Q8CG39	Q8CG39 rattus norv
22	21.8	7	13	Q8J320	Q8J320 gallus gall
23	21.8	8	2	Q9ZEZ9	Q9ZEZ9 buchnera ap
24	21.8	8	4	Q9BYV5	Q9BYV5 homo sapien
25	21.8	8	4	Q15895	Q15895 homo sapien
26	21.8	8	4	Q15890	Q15890 homo sapien
27	21.8	8	6	Q9BF82	Q9BF82 ursus arcto
28	21.8	8	6	Q9BFC2	Q9BFC2 macropus eu
29	21.8	8	6	Q9BF90	Q9BF90 tragelaphus
30	21.8	8	6	Q9BFB1	Q9BFB1 echinops te
31	21.8	8	6	Q9BFP3	Q9BFP3 megaptera n
32	21.8	8	6	Q9BFA1	Q9BFA1 atelies fusc
33	21.8	8	6	Q9BF87	Q9BF87 tapirus ind
34	21.8	8	6	Q9BFB9	Q9BFB9 euphractus
35	21.8	8	6	Q9BFB8	Q9BFB8 chaetophrac
36	21.8	8	6	Q9BFA0	Q9BFA0 macaca mula
37	21.8	8	6	Q9BFA8	Q9BFA8 loxodonta a
38	21.8	8	6	Q9BFA9	Q9BFA9 procavia ca
39	21.8	8	6	Q9BFB2	Q9BFB2 sorex arane
40	21.8	8	6	Q9BFB5	Q9BFB5 erinaceus c
41	21.8	8	6	Q9BFB6	Q9BFB6 myrmecophag
42	21.8	8	6	Q9BFB3	Q9BFB3 condylura c
43	21.8	8	6	Q9BFB8	Q9BFB8 equus cabal
44	21.8	8	6	Q9BFP5	Q9BFP5 rousettus l
45	21.8	8	6	Q9BFP9	Q9BFP9 hylobates c

## ALIGNMENTS

RESULT 1  
Q8IV87 PRELIMINARY; PRT; 8 AA.  
AC Q8IV87;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE DJ107712.2 (Serine palmitoyltransferase, long chain base subunit  
2-like (Aminotransferase 2), variant 1) (Fragment).  
GN SPTLC2L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Smith M.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL050320; CAD54807.1; -.  
DR GO; GO:0016740; F:transferase activity; IEA.  
KW Transferase.  
FT NON TER 1 1  
SQ SEQUENCE 8 AA; 308 MW; 8E533682CEBEB042 CRC64;  
Query Match 32.7%; Score 18; DB 4; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CC 2  
Db ||  
3 CC 4  
RESULT 2  
Q9SAY7 PRELIMINARY; PRT; 8 AA.  
ID Q9SAY7  
AC Q9SAY7;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Phosphoglucose isomerase (Fragment).  
 OS Diocesea tokoro.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spiromatophyta; Magnoliophyta; Liliopsida; Dioscoreales; Dioscoreaceae;  
 OC Diocesea.  
 OX NCBI\_TaxID=64475;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DT17-1;  
 RX MEDLINE=20279211; PubMed=10821191;  
 RA Terauchi K., Kahl G.;  
 RT "Rapid isolation of promoter sequences by TAIL-PCR: the 5'-flanking  
 regions of Pal and Pgi genes from yams (Dioscorea).";  
 RL Mol. Gen. Genet. 263:554-560 (2000).  
 DR EMBL; AB016716; BAA32235.1; -  
 DR GO; GO:0016853; F:isomerase activity; IEA.  
 KW Isomerase.  
 FT NON TER 8  
 SQ SEQUENCE 8 AA; 839 MW; F7B05731B5A1ADD6 CRC64;  
 Query Match 32.7%; Score 18; DB 10; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 6 SLIC 9  
 Db 5 TLIC 8  
 RESULT 3  
 Q9FSZ2  
 ID Q9FSZ2 PRELIMINARY; PRT; 9 AA.  
 AC Q9FSZ2;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein (Fragment).  
 OS Cicer arietinum (Chickpea) (Garbanzo).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.  
 OX NCBI\_TaxID=3827;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Castellana; TISSUE=Etisolated epicotyl;  
 RA Dopico B., Jimenez T., Labrador E.;  
 RT "cDNA clones expressed in etiolated Cicer arietinum epicotyls.";  
 RL Submitted (SAP-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ299069; CAC10216.1; -  
 DR GO; GO:0003674; F:protein-coding activity; IEA.  
 KW Hypothetical protein.  
 FT NON TER 1  
 SQ SEQUENCE 9 AA; 990 MW; 9441BDDAA7272EBE CRC64;  
 Query Match 32.7%; Score 18; DB 10; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CC 2  
 Db 1 CC 2  
 RESULT 4  
 Q8CG13  
 ID Q8CG13 PRELIMINARY; PRT; 9 AA.  
 AC Q8CG13;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A  
 DE (Fragment).  
 GN GRIN1A.  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;  
 RT "The mouse orthologue of the human ionotropic glutamate receptor-like  
 gene (GRIN1A) maps to mouse chromosome 9.";  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF462417; AAO15648.1; -  
 DR EMBL; AF462416; AAO15648.1; JOINED.  
 DR MGD; MGI:107282; Grin1a.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON TER 1  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C33B CRC64;  
 Query Match 32.7%; Score 18; DB 11; Length 9;  
 Best Local Similarity 60.0%; Pred. No. 1e+06;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 5 ESLIC 9  
 Db 2 EKFC 6  
 RESULT 5  
 Q9ELU7  
 ID Q9ELU7 PRELIMINARY; PRT; 9 AA.  
 AC Q9ELU7;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE X protein (Fragment).  
 GN X  
 OS Hepatitis B virus.  
 OC Viruses; Retroviruses; Hepadnaviridae; Orthohepadnavirus.  
 OX NCBI\_TaxID=10407;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2F-8;  
 RX MEDLINE=21213459; PubMed=11315638;  
 RA Ha-Lee Y.M., Lee J., Pyun H., Kim Y., Sohn J., Cho Y.J., Kim Y.;  
 RT "Sequence variation of Hepatitis B virus promoter regions in  
 persistently infected patients.";  
 RL Arch. Virol. 146:279-292 (2001).  
 DR EMBL; AF276526; AAG29993.1; -  
 DR NON TER 9  
 FT NON TER 9  
 SQ SEQUENCE 9 AA; 994 MW; CD0FDEBEA2D40DDD CRC64;  
 Query Match 32.7%; Score 18; DB 12; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CC 2  
 Db 6 CC 7  
 RESULT 6  
 Q86SF0  
 ID Q86SF0 PRELIMINARY; PRT; 9 AA.  
 AC Q86SF0;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Peroxisome proliferator-activated receptor alpha (Fragment).  
 GN PPARG.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22630144; PubMed=12745064;
RA Chew C.H., Samian M.R., Najimudin N., Tengku Muhammad T.S.;
RT "Molecular characterisation of six alternatively spliced variants and
a novel promoter in human peroxisome proliferator-activated receptor
alpha.";
RL Biochem. Biophys. Res. Commun. 305:235-243 (2003).
DR EMBL; AY258326; AA089521.1; -.
DR EMBL; AY258327; AA089522.1; -.
DR EMBL; AY258328; AA089523.1; -.
DR EMBL; AY258329; AA089524.1; -.
DR EMBL; AY258330; AA089525.1; -.
DR EMBL; AY258331; AA089526.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
SQ SEQUENCE 9 AA; 994 MW; DF8E3775BB01AAB2 CRC64;

Query Match 30.9%; Score 17; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 ESLIC 9
DB 5 ESPLC 9

RESULT 7
Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (Seg 4) cDNA, 3' end
(Fragment).
OS Influenzavirus A.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza A viruses.
OX NCBI_TaxID=197911;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81001892; PubMed=7407922;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500 (1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 29.1%; Score 16; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 2 CNEESLIC 9
DB 3 CN----IC 6

RESULT 8
O42564 PRELIMINARY; PRT; 7 AA.
AC O42564;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated voltage-gated sodium channel alpha subunit (Fragment).
GN SCN8A.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97442476; PubMed=9295353;
RA Plummer N.W., McBurney M.W., Meisler M.H.;
RT "Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
RL J. Biol. Chem. 272:24008-24015 (1997).
DR EMBL; U97673; AAB80916.1; -.
DR GO; GO:0005216; F:ion channel activity; IEA.
KW Ionic channel.
FT NON_TER
SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;

Query Match 29.1%; Score 16; DB 13; Length 7;
Best Local Similarity 66.7%; Pred. No. 1e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 LIC 9
DB 3 LVC 5

RESULT 9
P82440 PRELIMINARY; PRT; 9 AA.
AC P82440;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 42 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
tobacco culture.";
RL Planta 0:0-0 (2000).
CC -!- SUBCELLULAR LOCATION: CELL WALL.
CC -!- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON_TER
SQ SEQUENCE 9 AA; 1053 MW; 298CC9D2DSBB1B07 CRC64;

Query Match 27.3%; Score 15; DB 10; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EESL 7
DB 3 EESV 6

RESULT 10
O12096 PRELIMINARY; PRT; 9 AA.
AC O12096;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN TAT.

```

OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81439; AAB60832.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;  
Query Match 27.3%; Score 15; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CN 3  
Db 6 CN 7  
RESULT 11  
ID 012100 PRELIMINARY; PRT; 9 AA.  
AC 012100;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81441; AAB60836.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;  
Query Match 27.3%; Score 15; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CN 3  
Db 6 CN 7  
RESULT 12  
ID 012102 PRELIMINARY; PRT; 9 AA.  
AC 012102;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81442; AAB60838.1; -.  
FT NON\_TER 1

SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;  
Query Match 27.3%; Score 15; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CN 3  
Db 6 CN 7  
RESULT 13  
ID 012098 PRELIMINARY; PRT; 9 AA.  
AC 012098;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81440; AAB60835.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;  
Query Match 27.3%; Score 15; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CN 3  
Db 6 CN 7  
RESULT 14  
ID 012104 PRELIMINARY; PRT; 9 AA.  
AC 012104;  
DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE Tat protein (Fragment).  
GN TAT.  
OS Caprine arthritis encephalitis virus (CAEV).  
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.  
OX NCBI\_TaxID=11660;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;  
RT "dUTPase minus CAEV is attenuated for pathogenesis and accumulates G  
to A substitutions.";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U81443; AAB60840.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 922 MW; 21E8644EB7340EB8 CRC64;  
Query Match 27.3%; Score 15; DB 15; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 CN 3  
Db 6 CN 7

RESULT 15

Q8MJT7 PRELIMINARY; PRT; 9 AA.

AC Q8MJT7;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Hemopexin (Fragment).

OS Eulemur fulvus (brown lemur).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.

OX NCBI\_TaxID=13515;

RN [1]

RP SEQUENCE FROM N.A.

RA Wyner Y.M., Johnson S.E., Stumpf R., DeSalle R.;

RT "A genetic assessment of a red-fronted/white-collared lemur hybrid

RT zone at Andringitra, Madagascar."

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF258049; AAM43870.1; --

FT NON\_TER 1 1

FT NON\_TER 9 9

SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match 25.5%; Score 14; DB 6; Length 9;

Best Local Similarity 40.0%; Pred. No. 1e+06;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EESLI 8

Db ||| ::

2 EGGIL 6

Search completed: September 5, 2004, 11:05:41

Job time : 32.6667 secs

**This Page Blank (usp10)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:56:37 ; Search time 37.3333 Seconds  
(without alignments)  
68.114 Million cell updates/sec

Title: US-09-761-636A-9  
Perfect score: 55  
Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 231240

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Jan04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	4 AAU04528	AAU04528 VEGF base
2	50	90.9	9	4 AAU04552	AAU04552 VEGF base
3	49	89.1	9	4 AAU04553	AAU04553 VEGF base
4	46	83.6	8	4 AAU04525	AAU04525 VEGF base
5	43	78.2	8	4 AAU04539	AAU04539 VEGF base
6	42	76.4	8	4 AAU04541	AAU04541 VEGF base
7	41	74.5	8	4 AAU04538	AAU04538 VEGF base
8	39	70.9	8	4 AAU04540	AAU04540 VEGF base
9	35	63.6	8	4 AAU08451	AAU08451 Peptide A
10	33	60.0	8	4 AAU08460	AAU08460 Peptide C
11	33	60.0	9	6 ABR29819	ABR29819 Human can
12	33	60.0	9	6 ABR28797	ABR28797 Human can
13	33	60.0	9	6 ABR29456	ABR29456 Human can
14	33	60.0	9	6 ABR28814	ABR28814 Human can
15	33	60.0	9	6 ABR29789	ABR29789 Human can
16	33	60.0	9	6 ABR28619	ABR28619 Human can
17	33	60.0	9	6 ABR29608	ABR29608 Human can
18	33	60.0	9	6 ABR29220	ABR29220 Human can
19	33	60.0	9	6 ABR29572	ABR29572 Human can
20	33	60.0	9	6 ABR29383	ABR29383 Human can
21	31	56.4	6	2 AAR33979	AAR33979 Partial p
22	30	54.5	8	2 AAR24954	AAR24954 Conformat
23	30	54.5	8	3 AAY54526	AAY54526 Human CD4
24	29	52.7	9	6 ABR28842	ABR28842 Human can
25	28	50.9	9	2 AAU09329	AAU09329 FIV princ

26	28	50.9	9	2 AAY47045	AAY47045 Immunogen
27	28	50.9	9	6 ABR28618	ABR28618 Human can
28	28	50.9	9	6 ABR29242	ABR29242 Human can
29	27	49.1	8	2 AAR47420	AAR47420 PDGF-acti
30	27	49.1	8	2 AAR47390	AAR47390 PDGF-acti
31	27	49.1	8	2 AAR47421	AAR47421 PDGF-acti
32	27	49.1	8	2 AAR47419	AAR47419 PDGF-acti
33	27	49.1	9	2 AAU09330	AAU09330 FIV princ
34	27	49.1	9	5 ABG99560	ABG99560 Conus sp
35	26	47.3	8	2 AAR73351	AAR73351 Human TSH
36	26	47.3	8	2 AAR73350	AAR73350 Human TSH
37	26	47.3	8	3 AAY87160	AAY87160 Human sec
38	26	47.3	8	3 AAY57040	AAY57040 Feline im
39	26	47.3	8	4 AAE06137	AAE06137 Human gen
40	26	47.3	8	5 ABG33960	ABG33960 Human sec
41	26	47.3	9	2 AAR55115	AAR55115 Peptide p
42	26	47.3	9	2 AAU09328	AAU09328 FIV princ
43	26	47.3	9	2 AAW60376	AAW60376 Tumour ho
44	26	47.3	9	2 AAW93702	AAW93702 Human bre
45	26	47.3	9	2 AAY48648	AAY48648 Membrane

## ALIGNMENTS

RESULT 1  
AAU04528  
ID AAU04528 standard; protein; 9 AA.

XX AAU04528;

DT 26-SEP-2001 (first entry)

DE VEGF based bicyclic dimeric peptide #2.

XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.

OS Synthetic.

XX Key Location/Qualifiers

FT Disulfide-bond 1 /note= "A disulfide bond forms between residue 1 and  
FT residue 1 of an identical peptide to form a dimeric  
FT peptide, or between residue 1 and residue 17 of the  
FT sequence appearing as AAU04527 also forming a dimeric  
FT peptide"

FT Disulfide-bond 2..9 /note= "This bond cyclises the peptide"

WO200152875-A1.

26-JUL-2001.

PF 18-JAN-2001; 2001WO-US001533.

PR 18-JAN-2000; 2000US-0176293P.

PR 16-MAY-2000; 2000US-0204590P.

XX (LUDW-) LUDWIG INST CANCER RES.

PI Achen MG, Hughes RA, Stacker S, Cendron A;

XX WPI; 2001-442248/47.

PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
PT residues.

XX Claim 59; Page 32; 102pp; English.

XX The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 55; DB 4; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 9; Conservative 0; Mismatches 0;

QY 1 CCNEESLIC 9  
 |||||  
 Db 1 CCNEESLIC 9

RESULT 2  
 AAU04552  
 ID AAU04552 standard; peptide; 9 AA.  
 AC AAU04552;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX

VEGF based bicyclic dimeric peptide #9.

Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Disulfide-bond 1  
 FT /note= "A disulfide bond forms between residue 1 and  
 FT residue 17 of the sequence appearing as AAU04527, forming  
 FT a dimeric peptide"  
 FT Disulfide-bond 2..9  
 FT /note= "This bond cyclises the peptide"  
 FT

WO200152875-A1.  
 XX  
 PN  
 XX 26-JUL-2001.  
 XX  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR  
 PR 16-MAY-2000; 2000US-0204590P.

XX PA (LUDW-) LUDWIG INST CANCER RES.  
 XX PI Achen MG, Hughes RA, Stacker S, Cendron A;  
 XX WP1; 2001-442248/47.  
 DR  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX  
 XX Example 26; Page 49; 102pp; English.  
 PS  
 XX The sequence represents a dimeric bicyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy

XX SQ Sequence 9 AA;

Query Match 90.9%; Score 50; DB 4; Length 9;  
 Best Local Similarity 77.8%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 7; Conservative 2; Mismatches 0;

QY 1 CCNEESLIC 9  
 |||||  
 Db 1 CCNEESLIC 9

RESULT 3  
 AAU04553  
 ID AAU04553 standard; peptide; 9 AA.  
 XX  
 AC AAU04553;  
 XX  
 DT 26-SEP-2001 (first entry)  
 XX  
 DE VEGF based bicyclic dimeric peptide #10.  
 XX  
 KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 PH Key Location/Qualifiers  
 FT Disulfide-bond 1  
 FT /note= "A disulfide bond forms between residue 1 and

```

FT residue 17 of the sequence appearing as AAU04527, forming
FT a dimeric peptide"
FT Disulfide-bond 2..9 /note= "This bond cyclises the peptide"
FT
XX WO200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Example 26; Page 49; 102pp; English.
XX
XX The sequence represents a dimeric bicyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX metha carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis.
XX
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 9 AA;
XX
XX Query Match 89.1%; Score 49; DB 4; Length 9;
XX Best Local Similarity 77.8%; Pred. No. 1.4e+06;
XX Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CCNEESLIC 9
XX |||||
XX 1 CCNEETVIC 9
XX
XX RESULT 4
XX AAU04525
XX ID AAU04525 standard; peptide; 8 AA.
XX
XX AC AAU04525;
XX
XX DT 26-SEP-2001 (first entry)

```

```

XX VEGF based monocyclic peptide 2.
XX
XX Human; VEGF; vascular endothelial growth factor; angiogenesis;
XX neovascularisation; lymphangiogenesis; psoriasis; tumour;
XX diabetes induced neovascular sequelae; rheumatoid arthritis;
XX diabetic retinopathy; chronic inflammation; cyclic.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Disulfide-bond 1..8 /note= "This bond cyclises the peptide"
XX
XX WO200152875-A1.
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US001533.
XX
XX 18-JAN-2000; 2000US-0176293P.
XX 16-MAY-2000; 2000US-0204590P.
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Achen MG, Hughes RA, Stackler S, Cendron A;
XX WPI; 2001-442248/47.
XX
XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,
XX or lymphangiogenesis, is produced by cyclizing a peptide loop fragment
XX from an exposed loop of a growth factor protein by oxidizing the cysteine
XX residues.
XX
XX Claim 49; Page 32; 102pp; English.
XX
XX The sequence represents a monomeric monocyclic peptide of the invention,
XX whose 3-dimensional structure is modelled on the expose loop of human
XX VEGF (vascular endothelial growth factor). The invention relates to a
XX method of producing a monomeric monocyclic peptide by a measuring beta-
XX metha carbon separation distances on opposite antiparallel strands of a
XX peptide loop fragment from an exposed loop of a growth factor protein and
XX cyclising the peptide by oxidising the cysteine residues. The monocyclic
XX peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic
XX peptides) and a cyclic peptide with at least one amino acid deleted prior
XX to cyclisation are used to interfere with angiogenesis.
XX
XX neovascularisation or lymphangiogenesis in a mammal with a condition
XX characterised by angiogenesis, neovascularisation or lymphangiogenesis.
XX The condition is diabetic retinopathy, psoriasis, arthropathy,
XX hemangioma, vascularised malignant or benign tumour, post-recovery
XX cerebrovascular accident, post-angioplasty restenosis, head, heat or cold
XX trauma, substance-induced neovascularisation of the liver, excessive
XX hormone-related angiogenic dysfunction, diabetes induced neovascular
XX sequelae, hypertension induced neovascular sequelae, or chronic liver
XX infection. The peptides are also used to modulate vascular permeability
XX in a mammal (the mammal has a condition characterised by fluid
XX accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,
XX or brain. The peptides are used to image blood vessels and lymphatic
XX vasculature. The monomeric and bicyclic peptides are used to interfere
XX with at least one biological activity induced by VEGF, VEGF-C or -D and
XX are also used in combination with an anti-inflammatory agent, to treat a
XX chronic inflammation, especially rheumatoid arthritis, psoriasis and
XX diabetic retinopathy
XX
XX Sequence 8 AA;
XX
XX Query Match 83.6%; Score 46; DB 4; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 2 CNEESLIC 9
XX |||||
XX 1 CNEESLIC 8
XX
XX QY
XX DB

```

RESULT 5  
AAU04539 ID AAU04539 standard; peptide; 8 AA.  
XX AC AAU04539;  
XX DT 26-SEP-2001 (first entry)  
XX DE VEGF based monocyclic peptide 17.  
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"  
XX WO200152875-A1.  
XX PD 26-JUL-2001.  
XX PF 18-JAN-2001; 2001WO-US001533.  
XX PR 18-JAN-2000; 2000US-0176293P.  
XX PR 16-MAY-2000; 2000US-0204590P.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;  
XX WPI; 2001-442248/47.  
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
PT residues.  
XX Example 25; Page 47; 102pp; English.  
XX The sequence represents a monomeric monocyclic peptide of the invention,  
CC whose 3-dimensional structure is modelled on the expose loop of human  
CC VEGFD (vascular endothelial growth factor). The invention relates to a  
CC method of producing a monomeric monocyclic peptide by a measuring beta-  
CC beta carbon separation distances on opposite antiparallel strands of a  
CC peptide loop fragment from an exposed loop of a growth factor protein and  
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
CC to cyclisation are used to interfere with angiogenesis,  
CC neovascularisation or lymphangiogenesis in a mammal with a condition  
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
CC hemangioma, vascularised malignant or benign tumour, post-recovery  
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
CC trauma, substance-induced neovascularisation of the liver, excessive  
CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
CC infection. The peptides are also used to modulate vascular permeability  
CC in a mammal (the mammal has a condition characterised by fluid  
CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
CC or brain. The peptides are used to image blood vessels and lymphatic  
CC vasculature. The monomeric and bicyclic peptides are used to interfere  
CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
CC are also used in combination with an anti-inflammatory agent, to treat a  
CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
CC diabetic retinopathy

SQ Sequence 8 AA;  
Query Match 78.2%; Score 43; DB 4; Length 8;  
Best Local Similarity 87.5%; Pred. NO. 1.4e+06;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 CNEESLIC 9  
DB 1 CNEETLIC 8  
RESULT 6  
AAU04541 ID AAU04541 standard; peptide; 8 AA.  
XX AC AAU04541;  
XX DT 26-SEP-2001 (first entry)  
XX DE VEGF based monocyclic peptide 19.  
XX KW Human; VEGF; vascular endothelial growth factor; angiogenesis;  
KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
KW diabetic retinopathy; chronic inflammation; cyclic.  
XX OS Synthetic.  
XX FH Key Location/Qualifiers  
FT Disulfide-bond 1..8 /note= "This bond cyclises the peptide"  
XX WO200152875-A1.  
XX PD 26-JUL-2001.  
XX PF 18-JAN-2001; 2001WO-US001533.  
XX PR 18-JAN-2000; 2000US-0176293P.  
XX PR 16-MAY-2000; 2000US-0204590P.  
XX PA (LUDW-) LUDWIG INST CANCER RES.  
XX PI Achen MG, Hughes RA, Stacker S, Cendron A;  
XX WPI; 2001-442248/47.  
XX PT Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
PT residues.  
XX Example 25; Page 47; 102pp; English.  
XX The sequence represents a monomeric monocyclic peptide of the invention,  
CC whose 3-dimensional structure is modelled on the expose loop of human  
CC VEGFD (vascular endothelial growth factor). The invention relates to a  
CC method of producing a monomeric monocyclic peptide by a measuring beta-  
CC beta carbon separation distances on opposite antiparallel strands of a  
CC peptide loop fragment from an exposed loop of a growth factor protein and  
CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
CC to cyclisation are used to interfere with angiogenesis,  
CC neovascularisation or lymphangiogenesis in a mammal with a condition  
CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
CC hemangioma, vascularised malignant or benign tumour, post-recovery  
CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
CC trauma, substance-induced neovascularisation of the liver, excessive  
CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
CC infection. The peptides are also used to modulate vascular permeability



CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 8 AA;

Query Match 76.4%; Score 42; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9  
 DB 1 CNEESVVC 8  
 |||::|

RESULT 7  
 AAU04538  
 ID AAU04538 standard; peptide; 8 AA.  
 XX  
 AC AAU04538;  
 DT 26-SEP-2001 (first entry)  
 DE VEGF based monocyclic peptide 16.  
 XX  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 FH Disulfide-bond 1..8  
 FT /note= "This bond cyclises the peptide"  
 XX  
 PN WO200152875-A1.  
 XX 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 PS The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis.

CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy  
 XX  
 SQ Sequence 8 AA;

Query Match 74.5%; Score 41; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CNEESLIC 9  
 DB 1 CNEESLIC 8  
 |||::|

RESULT 8  
 AAU04540  
 ID AAU04540 standard; peptide; 8 AA.  
 XX  
 AC AAU04540;  
 XX 26-SEP-2001 (first entry)  
 XX VEGF based monocyclic peptide 18.  
 DE  
 XX Human; VEGF; vascular endothelial growth factor; angiogenesis;  
 KW neovascularisation; lymphangiogenesis; psoriasis; tumour;  
 KW diabetes induced neovascular sequelae; rheumatoid arthritis;  
 KW diabetic retinopathy; chronic inflammation; cyclic.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 FH Disulfide-bond 1..8  
 FT /note= "This bond cyclises the peptide"  
 XX  
 PN WO200152875-A1.  
 XX 26-JUL-2001.  
 XX 18-JAN-2001; 2001WO-US001533.  
 XX 18-JAN-2000; 2000US-0176293P.  
 PR 16-MAY-2000; 2000US-0204590P.  
 XX (LUDW-) LUDWIG INST CANCER RES.  
 PA Achen MG, Hughes RA, Stacker S, Cendron A;  
 PI WPI; 2001-442248/47.  
 XX Novel monomeric monocyclic peptide, used to interfere with angiogenesis,  
 PT or lymphangiogenesis, is produced by cyclizing a peptide loop fragment  
 PT from an exposed loop of a growth factor protein by oxidizing the cysteine  
 PT residues.  
 XX Example 25; Page 47; 102pp; English.  
 PS The sequence represents a monomeric monocyclic peptide of the invention,  
 CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGF (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis.

CC whose 3-dimensional structure is modelled on the expose loop of human  
 CC VEGFD (vascular endothelial growth factor). The invention relates to a  
 CC method of producing a monomeric monocyclic peptide by a measuring beta-  
 CC beta carbon separation distances on opposite antiparallel strands of a  
 CC peptide loop fragment from an exposed loop of a growth factor protein and  
 CC cyclising the peptide by oxidising the cysteine residues. The monocyclic  
 CC peptides, dimeric bicyclic peptides (comprising 2 linked monocyclic  
 CC peptides) and a cyclic peptide with at least one amino acid deleted prior  
 CC to cyclisation are used to interfere with angiogenesis,  
 CC neovascularisation or lymphangiogenesis in a mammal with a condition  
 CC characterised by angiogenesis, neovascularisation or lymphangiogenesis.  
 CC The condition is diabetic retinopathy, psoriasis, arthropathy,  
 CC hemangioma, vascularised malignant or benign tumour, post-recovery  
 CC cerebrovascular accident, post-angioplasty restenosis, head, heat or cold  
 CC trauma, substance-induced neovascularisation of the liver, excessive  
 CC hormone-related angiogenic dysfunction, diabetes induced neovascular  
 CC sequelae, hypertension induced neovascular sequelae, or chronic liver  
 CC infection. The peptides are also used to modulate vascular permeability  
 CC in a mammal (the mammal has a condition characterised by fluid  
 CC accumulation in peripheral limbs or in lungs, peritoneal cavity, pleura,  
 CC or brain. The peptides are used to image blood vessels and lymphatic  
 CC vasculature. The monomeric and bicyclic peptides are used to interfere  
 CC with at least one biological activity induced by VEGF, VEGF-C or -D and  
 CC are also used in combination with an anti-inflammatory agent, to treat a  
 CC chronic inflammation, especially rheumatoid arthritis, psoriasis and  
 CC diabetic retinopathy

XX SQ Sequence 8 AA;

Query Match 70.9%; Score 39; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 1.4e+06;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CNEESLIC 9  
 Db |||:| |  
 1 CNEDSFIC 8

RESULT 9  
 AAU08451

ID AAU08451 standard; peptide; 8 AA.

AC AAU08451;

DT 21-NOV-2001 (first entry)

DE Peptide A6 encoded by human VEGF-A forward primer A6-F.

XX Human; vascular endothelial growth factor; VEGF-A; vasculogenesis;  
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;  
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;  
 KW primer; mutant; mutein.

XX Homo sapiens.  
 OS Synthetic.

PN WO200162942-A2.

PD 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US006113.

XX 25-FEB-2000; 2000US-0185205P.

PR 18-MAY-2000; 2000US-0205331P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA OY.

XX Alitalo K, Jeltsch MM;

XX WPI; 2001-536640/59.

DR N-PSDB; AAS12807.

XX

PT Polypeptides that bind cellular receptors for vascular endothelial growth  
 PT factors, polynucleotides encoding them.

XX Claim 9; Fig 7C; 26lpp; English.

XX The present invention relates to polypeptides that bind cellular  
 CC receptors for vascular endothelial growth factors (VEGFs), the  
 CC polynucleotides encoding them, and their use for identifying agents that  
 CC modulate interactions between VEGFs and their receptors. VEGFs and their  
 CC receptors play an important role in vasculogenesis, the development of  
 CC the embryonic vasculature from early differentiating endothelial cells  
 CC and angiogenesis, the process of forming new blood vessels from pre-  
 CC existing ones. Modulators of interactions between VEGF and its receptors  
 CC may be used to treat dysfunction of the endothelial cell regulatory  
 CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid  
 CC proliferative retinopathies, age-related macular degeneration, psoriasis,  
 CC arthritis and psoriasis. The polypeptides of the invention exhibit unique  
 CC receptor binding profiles compared to known naturally occurring VEGFs.  
 CC AAU08446-AAU08454 represent the peptides A1-A9 which are encoded by human  
 CC VEGF-A forward primers used in the methods of the present invention

XX SQ Sequence 8 AA;

Query Match 63.6%; Score 35; DB 4; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCNEESL 7  
 Db |||:| |  
 2 CCNDEGL 8

RESULT 10

AAU08460

ID AAU08460 standard; peptide; 8 AA.

XX AAU08460;

DT 21-NOV-2001 (first entry)

DE Peptide C6 encoded by human VEGF-C forward primer C6-F.

XX Human; vascular endothelial growth factor; VEGF-C; vasculogenesis;  
 KW angiogenesis; blood vessel; cancer; proliferative retinopathy; psoriasis;  
 KW age-related macular degeneration; rheumatoid arthritis; cardiovascular;  
 KW primer; mutant; mutein.

XX Homo sapiens.

OS Synthetic.

PN WO200162942-A2.

XX 30-AUG-2001.

XX 26-FEB-2001; 2001WO-US006113.

XX 25-FEB-2000; 2000US-0185205P.

PR 18-MAY-2000; 2000US-0205331P.

XX (LUDW-) LUDWIG INST CANCER RES.

PA (LICN) LICENTIA OY.

XX Alitalo K, Jeltsch MM;

XX WPI; 2001-536640/59.

DR N-PSDB; AAS12826.

XX Polypeptides that bind cellular receptors for vascular endothelial growth  
 PT factors, polynucleotides encoding them.

XX Claim 9; Fig 7C; 26lpp; English.

XX The present invention relates to polypeptides that bind cellular

CC receptors for vascular endothelial growth factors (VEGFs), the  
 CC polynucleotides encoding them, and their use for identifying agents that  
 CC modulate interactions between VEGFs and their receptors. VEGFs and their  
 CC receptors play an important role in vasculogenesis, the development of  
 CC the embryonic vasculature from early differentiating endothelial cells  
 CC and angiogenesis, the process of forming new blood vessels from pre-  
 CC existing ones. Modulators of interactions between VEGF and its receptors  
 CC system. Such disorders include cancers, abnormal angiogenesis, rheumatoid  
 CC proliferative retinopathies, age-related macular degeneration, arthritis  
 CC and psoriasis. The polypeptides of the invention exhibit unique  
 CC receptor binding profiles compared to known naturally occurring VEGFs.  
 CC AAU08455-AAU08463 represent the peptides C1-C9 which are encoded by human  
 CC VEGF-C forward primers used in the methods of the present invention  
 XX  
 SQ Sequence 8 AA;

Query Match 60.0%; Score 33; DB 4; Length 8;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESL 7  
 DB 2 CCNSEGL 8

RESULT 11  
 ABR29819  
 ID ABR29819 standard; peptide; 9 AA.

XX AC ABR29819;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 192P2G7 HLA peptide #1263.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.  
 XX PR 10-APR-2001; 2001US-0282739P.  
 XX PR 10-APR-2001; 2001US-0283112P.  
 XX PR 25-APR-2001; 2001US-0286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 XX PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.

XX DR New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.

XX PS Claim 13; Page 431; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention  
 XX  
 SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCNEESL 7  
 DB 1 CCNAEAL 7

RESULT 12  
 ABR28797  
 ID ABR28797 standard; peptide; 9 AA.

XX AC ABR28797;  
 XX DT 19-MAY-2003 (first entry)  
 XX DE Human cancer-related protein 192P2G7 HLA peptide #241.  
 XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;  
 XX human leukocyte antigen.  
 XX OS Homo sapiens.  
 XX PN WO200283921-A2.  
 XX PD 24-OCT-2002.

XX PF 10-APR-2002; 2002WO-US011654.  
 XX PR 10-APR-2001; 2001US-0282739P.  
 XX PR 10-APR-2001; 2001US-0283112P.  
 XX PR 25-APR-2001; 2001US-0286630P.  
 XX PA (AGEN-) AGENSYS INC.  
 XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;  
 XX PI Morrison K, Morrison RK, Raitano AB;  
 XX WPI; 2003-075555/07.

XX DR New composition comprising a substance that modulates the structure of  
 PT proteins and polynucleotides, useful for therapeutic, prognostic and  
 PT diagnostic reagents for eliciting cellular or humoral immune response in  
 PT cancer patients.

XX PS Claim 13; Page 419; 1021pp; English.

XX CC The present invention relates to novel human cancer-related genes and  
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and  
 CC proteins are useful for eliciting a humoral or cellular immune response.  
 CC The genes are useful as probes and primers for the amplification and/or  
 CC detection of genes, mRNAs or their fragments, as reagents for the  
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of  
 CC directing the expression of the protein, as tools for modulating or  
 CC inhibiting the expression of genes and/or translation of transcripts, and  
 CC as therapeutic agents. The proteins and peptides are useful as  
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present  
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example  
 CC from the invention

XX SQ Sequence 9 AA;

Query Match 60.0%; Score 33; DB 6; Length 9;  
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 13
ID ABR29456 standard; peptide; 9 AA.
XX
AC ABR29456;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #900.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 427; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 14
ID ABR28814 standard; peptide; 9 AA.
XX
AC ABR28814;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #258.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
XX
OS Homo sapiens.
XX
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 419; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of the protein, as tools for modulating or
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 9 AA;
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCNEESL 7
Db      1 CCNAEAL 7

RESULT 15
ID ABR29789 standard; peptide; 9 AA.
XX
AC ABR29789;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 192P2G7 HLA peptide #1233.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
human leukocyte antigen.
XX
OS Homo sapiens.

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XX WO200283921-A2.
XX
XX
PD 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 431; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
XX Sequence 9 AA;
SQ
Query Match 60.0%; Score 33; DB 6; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCNEESL 7
Db 3 CCNAEAL 9

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OM protein - protein search, using sw model

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## SUMMARIES

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4	46	83.6	8	9	US-09-761-636A-6	Sequence 6, Appli
5	43	78.2	8	9	US-09-761-636A-20	Sequence 20, Appl
6	42	76.4	8	9	US-09-761-636A-22	Sequence 22, Appl
7	41	74.5	8	9	US-09-761-636A-19	Sequence 19, Appl
8	39	70.9	8	9	US-09-761-636A-21	Sequence 21, Appl
9	35	63.6	8	9	US-09-795-006A-133	Sequence 133, App
10	33	60.0	8	9	US-09-795-006A-142	Sequence 142, App
11	29	52.7	5	12	US-10-436-549-605	Sequence 605, App
12	27	49.1	9	14	US-10-072-602B-292	Sequence 292, App
13	26	47.3	8	10	US-09-984-271-199	Sequence 199, App
14	26	47.3	8	12	US-09-984-276-199	Sequence 199, App
15	26	47.3	8	15	US-10-149-138-2497	Sequence 2497, Ap

16	26	47.3	8	15	US-10-149-138-2515	Sequence 2515, Ap
17	26	47.3	8	16	US-10-149-138-2497	Sequence 2497, Ap
18	26	47.3	8	16	US-10-149-138-2515	Sequence 2515, Ap
19	26	47.3	9	9	US-09-765-086-93	Sequence 93, Appl
20	26	47.3	9	14	US-10-264-374-93	Sequence 93, Appl
21	26	47.3	9	14	US-10-375-992-93	Sequence 93, Appl
22	26	47.3	9	14	US-10-286-457-109	Sequence 109, App
23	26	47.3	9	15	US-10-149-138-2516	Sequence 2516, Ap
24	26	47.3	9	15	US-10-149-138-3064	Sequence 3064, Ap
25	26	47.3	9	15	US-10-149-138-4029	Sequence 4029, Ap
26	26	47.3	9	15	US-10-149-138-4156	Sequence 4156, Ap
27	26	47.3	9	16	US-10-264-374-93	Sequence 93, Appl
28	26	47.3	9	16	US-10-149-138-2516	Sequence 2516, Ap
29	26	47.3	9	16	US-10-149-138-3064	Sequence 3064, Ap
30	26	47.3	9	16	US-10-149-138-4029	Sequence 4029, Ap
31	26	47.3	9	16	US-10-149-138-4156	Sequence 4156, Ap
32	26	47.3	9	16	US-10-375-992-93	Sequence 93, Appl
33	25	45.5	8	12	US-10-363-208-108	Sequence 108, App
34	25	45.5	8	14	US-10-012-806A-13	Sequence 13, Appl
35	25	45.5	8	14	US-10-012-806A-15	Sequence 15, Appl
36	25	45.5	8	14	US-10-012-806A-19	Sequence 19, Appl
37	25	45.5	8	14	US-10-012-806A-37	Sequence 37, Appl
38	25	45.5	9	10	US-09-942-052-46	Sequence 46, Appl
39	25	45.5	9	10	US-09-942-052-126	Sequence 126, App
40	25	45.5	9	10	US-09-942-052-216	Sequence 216, App
41	25	45.5	9	14	US-10-072-602B-509	Sequence 509, App
42	25	45.5	9	14	US-10-012-806A-11	Sequence 11, Appl
43	25	45.5	9	14	US-10-286-457-354	Sequence 354, App
44	24	43.6	8	9	US-09-826-290-367	Sequence 367, App
45	24	43.6	8	14	US-10-006-869-917	Sequence 917, App

## ALIGNMENTS

RESULT 1  
US-09-761-636A-9  
; Sequence 9, Application US/09761636A  
; Patent No. US20020085218A1  
; GENERAL INFORMATION:  
; APPLICANT: ACHEN, Marc  
; APPLICANT: STACKER, Steven  
; APPLICANT: HUGHES, Richard  
; APPLICANT: CENDRON, Angela  
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR  
; FILE REFERENCE: 1064/48505 Achen et al  
; CURRENT APPLICATION NUMBER: US/09/761,636A  
; CURRENT FILING DATE: 2001-01-18  
; PRIOR APPLICATION NUMBER: US 60/176,293  
; PRIOR FILING DATE: 2000-01-18  
; PRIOR APPLICATION NUMBER: US 60/204,590  
; PRIOR FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-761-636A-9

Query Match 100.0%; Score 55; DB 9; Length 9;  
Best Local Similarity 100.0%; Pred.No. 1.2e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9  
Db 1 CCNEESLIC 9

RESULT 2  
US-09-761-636A-33  
; Sequence 33, Application US/09761636A  
; Patent No. US20020085218A1

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; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; TYPE: PRT
; LENGTH: 9
; ORGANISM: synthetic construct
US-09-761-636A-33
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Query Match 90.9%; Score 50; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CNEESLIC 9
Db 1 CNEESLIC 9
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RESULT 3
US-09-761-636A-34
; Sequence 34, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-34
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Query Match 89.1%; Score 49; DB 9; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.2e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CNEESLIC 9
Db 1 CNEETVIC 9
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RESULT 4
US-09-761-636A-6
; Sequence 6, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
```

```
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-761-636A-6
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Query Match 83.6%; Score 46; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 CNEESLIC 9
Db 1 CNEESLIC 8
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RESULT 5
US-09-761-636A-20
; Sequence 20, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-20
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Query Match 78.2%; Score 43; DB 9; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 2 CNEESLIC 9
Db 1 CNEETLIC 8
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RESULT 6
US-09-761-636A-22
; Sequence 22, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
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; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-22

Query Match          76.4%; Score 42; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESWVC 8

RESULT 7
US-09-761-636A-19
; Sequence 19, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-19

Query Match          74.5%; Score 41; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESLIC 8

RESULT 8
US-09-761-636A-21
; Sequence 21, Application US/09761636A
; Patent No. US20020065218A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc
; APPLICANT: STACKER, Steven
; APPLICANT: HUGHES, Richard
; APPLICANT: CENDRON, Angela
; TITLE OF INVENTION: VEGF-D/VEGF-C/VEGF PEPTIDOMIMETIC INHIBITOR
; FILE REFERENCE: 1064/48505 Achen et al
; CURRENT APPLICATION NUMBER: US/09/761,636A
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 60/176,293
; PRIOR FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: US 60/204,590
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
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; SEQ ID NO 21
; LENGTH: 8
; TYPE: PRT
; ORGANISM: synthetic construct
US-09-761-636A-21

Query Match          70.9%; Score 39; DB 9; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.2e+06;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CNEESLIC 9
Db 1 CNEESFIC 8

RESULT 9
US-09-795-006A-133
; Sequence 133, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alicalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-795-006A-133

Query Match          63.6%; Score 35; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCNEESL 7
Db 2 CCNDEGL 8

RESULT 10
US-09-795-006A-142
; Sequence 142, Application US/09795006A
; Patent No. US20020151680A1
; GENERAL INFORMATION:
; APPLICANT: Alicalo et al
; TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR
; FILE REFERENCE: 28967/35977B
; CURRENT APPLICATION NUMBER: US/09/795,006A
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: US 60/205,331
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: US 60/185,205
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 142
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
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; OTHER INFORMATION: peptide
US-09-795-006A-142

Query Match      60.0%; Score 33; DB 9; Length 8;
Best Local Similarity 71.4%; Pred. NO. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CCNERSL 7
      |||||
Db      2 CCNSEGL 8

RESULT 11
US-10-436-549-605
; Sequence 605, Application US/10436549
; Publication No. US20040038307A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank D.
; APPLICANT: Meng, Dr. Xun
; APPLICANT: Chan, John W.
; APPLICANT: Zhang, Shengsheng
; APPLICANT: Benkovic, Stephen J.
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: ENGE-P01-001
; CURRENT APPLICATION NUMBER: US/10/436,549
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,626
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/393,233
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,235
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,211
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,280
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,197
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/393,223
; PRIOR FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 60/430,948
; PRIOR FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/433,319
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: 60/393,137
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 614
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 605
; LENGTH: 5
; TYPE: PRT
; ORGANISM: human
US-10-436-549-605

Query Match      52.7%; Score 29; DB 12; Length 5;
Best Local Similarity 100.0%; Pred. NO. 1.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCNE 4
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Db      2 CCNE 5

RESULT 12
US-10-072-602B-292
; Sequence 292, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J, Michael
```

```
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Conus dalli
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(9)
; OTHER INFORMATION: Xaa at residue 1 is Glu or gamma-carboxy-Glu; Xaa at residue 5 is Tyr,
; OTHER INFORMATION: Trp (D or L) or bromo-Trp (D or L); Xaa at residue 4 is Tyr,
; OTHER INFORMATION: 125I-Tyr, mono-iodo-Tyr, di-iodo-Tyr, O-sulpho-Tyr or
; OTHER INFORMATION: O-phospho-Tyr
US-10-072-602B-292

Query Match      49.1%; Score 27; DB 14; Length 9;
Best Local Similarity 44.4%; Pred. NO. 1.2e+06;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      1 CCNERSLIC 9
      |||||
Db      1 CCXXXKLC 9

RESULT 13
US-09-984-271-199
; Sequence 199, Application US/09984271
; Publication No. US20030040088A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins
; FILE REFERENCE: PZ030PI
; CURRENT APPLICATION NUMBER: US/09/984,271
; CURRENT FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: 09/482,273
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: PCT/US99/15849
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,922
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/092,956
; PRIOR FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 267
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-271-199

Query Match      47.3%; Score 26; DB 10; Length 8;
Best Local Similarity 75.0%; Pred. NO. 1.2e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCNE 4
      |||
Db      1 CCNQ 4
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## RESULT 14

US-09-984-276-199  
; Sequence 199, Application US/09984276  
; Publication No. US20030017500A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 71 Human Secreted Proteins  
; FILE REFERENCE: P2030P1  
; CURRENT APPLICATION NUMBER: US/09/984,276  
; CURRENT FILING DATE: 2001-10-29  
; PRIOR APPLICATION NUMBER: 09/482,273  
; PRIOR FILING DATE: 2000-01-13  
; PRIOR APPLICATION NUMBER: 60/092,921  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/092,922  
; PRIOR FILING DATE: 1998-07-15  
; PRIOR APPLICATION NUMBER: 60/092,956  
; PRIOR FILING DATE: 1998-07-15  
; NUMBER OF SEQ ID NOS: 267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 199  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-984-276-199

Query Match 47.3%; Score 26; DB 12; Length 8;  
Best Local Similarity 75.0%; Pred.No. 1.2e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNE 4  
Db 1 CCNQ 4

## RESULT 15

US-10-149-138-2497  
; Sequence 2497, Application US/10149138  
; Publication No. US20040018971A1  
; GENERAL INFORMATION:  
; APPLICANT: Fikes, John  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Keogh, Elissa  
; TITLE OF INVENTION: Inducing Cellular Immune Responses to  
; FILE REFERENCE: 2060.0140001  
; CURRENT APPLICATION NUMBER: US/10/149,138  
; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: PCT/US00/33591  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/458,299  
; PRIOR FILING DATE: 1999-12-11  
; NUMBER OF SEQ ID NOS: 4641  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2497  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptide  
US-10-149-138-2497

Query Match 47.3%; Score 26; DB 15; Length 8;  
Best Local Similarity 60.0%; Pred.No. 1.2e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCNEE 5

Db 1 CCHQ 5

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Job time : 36.6667 secs

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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:01:38 ; Search time 12 Seconds  
(without alignments)  
38.719 Million cell updates/sec

Title: US-09-761-636A-9  
Perfect score: 55  
Sequence: 1 CCNEESLIC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 89883

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	27	49.1	8	5	PCT-US93-05325-31
5	27	49.1	8	5	PCT-US93-05325-32
6	26	47.3	8	4	US-09-089-878-3
7	26	47.3	8	4	US-09-482-273-199
8	26	47.3	9	3	US-09-258-754-13
9	26	47.3	9	3	US-09-139-802-93
10	26	47.3	9	3	US-09-042-107-13
11	26	47.3	9	4	US-09-659-786-93
12	26	47.3	9	4	US-08-926-914-93
13	26	47.3	9	4	US-09-722-250D-13
14	25	45.5	8	1	US-08-107-411-7
15	25	45.5	8	1	US-08-397-633A-100
16	25	45.5	8	3	US-09-258-754-49
17	25	45.5	8	3	US-09-042-107-49
18	25	45.5	8	4	US-09-722-250D-49
19	25	45.5	9	4	US-09-535-852-1205
20	24	43.6	4	3	US-08-750-142B-17
21	24	43.6	5	4	US-09-708-606-22
22	24	43.6	6	4	US-09-708-606-8
23	24	43.6	6	4	US-09-708-606-26
24	24	43.6	7	3	US-08-750-142B-37
25	24	43.6	7	4	US-09-717-364A-32
26	24	43.6	7	4	US-09-708-606-11
27	24	43.6	8	4	US-09-187-859-917

28	24	43.6	8	4	US-09-839-542B-917
29	24	43.6	8	4	US-09-708-606-20
30	24	43.6	9	4	US-09-535-852-927
31	24	43.6	9	4	US-09-708-606-10
32	23	41.8	7	3	US-08-973-551-14
33	23	41.8	8	2	US-08-520-535-3
34	23	41.8	8	2	US-09-079-432-3
35	23	41.8	8	3	US-09-258-754-33
36	23	41.8	8	3	US-09-258-754-42
37	23	41.8	8	3	US-09-258-754-214
38	23	41.8	8	3	US-09-042-107-33
39	23	41.8	8	3	US-09-042-107-42
40	23	41.8	8	3	US-09-042-107-214
41	23	41.8	8	3	US-08-160-604-79
42	23	41.8	8	3	US-08-160-604-80
43	23	41.8	8	4	US-09-314-268-61
44	23	41.8	8	4	US-09-314-268-62
45	23	41.8	8	4	US-09-314-268-63

ALIGNMENTS

RESULT 1  
US-09-100-409A-27  
; Sequence 27, Application US/09100409A  
; Patent No. 6090388  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND  
; TITLE OF INVENTION: IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,409A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 1151-4154  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-751-6800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
US-09-100-409A-27

Query Match 54.5%; Score 30; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 3e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCNEESLIC 9  
||:|:|:  
DB 1 CNOGSFLC 8

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RESULT 2
PCT-US93-05325-2
; Sequence 2, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: PCT-2679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-2446
; TELEFAX: (415) 859-3880
; TELEX: 334486
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-05325-2

Query Match 49.1%; Score 27; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
Db 3 CCNTSS 8

RESULT 3
PCT-US93-05325-30
; Sequence 30, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: PCT-2679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-2446
; TELEFAX: (415) 859-3880
; TELEX: 334486
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-05325-2
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CLARK, JANET P.
; REGISTRATION NUMBER: 34,799
; REFERENCE/DOCKET NUMBER: PCT-2679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 859-2446
; TELEFAX: (415) 859-3880
; TELEX: 334486
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /note= "This position is modified
; OTHER INFORMATION: with Acn."
; PCT-US93-05325-30

Query Match 49.1%; Score 27; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6
Db 3 CCNTSS 8

RESULT 4
PCT-US93-05325-31
; Sequence 31, Application PC/TUS9305325
; GENERAL INFORMATION:
; APPLICANT: SRI, INTERNATIONAL
; TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
; TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
; ADDRESSEE: COUNSEL
; STREET: 333 Ravenswood Avenue
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05325
; FILING DATE: 19930603
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,497
; FILING DATE: 05-JUN-1992
; ATTORNEY/AGENT INFORMATION:
```

NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: PCT-2679  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 859-2446  
 TELEFAX: (415) 859-3880  
 TELEX: 334486  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: both  
 MOLECULE TYPE: peptide  
 PCT-US93-05325-31

Query Match 49.1%; Score 27; DB 5; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 3e+05;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6  
 |||||  
 Db 3 CCNTSS 8

## RESULT 5

PCT-US93-05325-32  
 Sequence 32, Application PC/TUS9305325  
 GENERAL INFORMATION:

APPLICANT: SRI, INTERNATIONAL  
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS  
 TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: SRI INTERNATIONAL ATTN: INTELLECTUAL PROPERTY  
 ADDRESSEE: COUNSEL  
 STREET: 333 Ravenswood Avenue  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94025

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US93/05325  
 FILING DATE: 19930603

## CLASSIFICATION:

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/894,497  
 FILING DATE: 05-JUN-1992

## ATTORNEY/AGENT INFORMATION:

NAME: CLARK, JANET P.  
 REGISTRATION NUMBER: 34,799  
 REFERENCE/DOCKET NUMBER: PCT-2679  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 859-2446  
 TELEFAX: (415) 859-3880  
 TELEX: 334486

## INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FEATURE:

NAME/KEY: Disulfide-bond

LOCATION: 3-4

OTHER INFORMATION: /note= "This position has disulfide

OTHER INFORMATION: bond to corresponding position of identical

OTHER INFORMATION: sequence."

PCT-US93-05325-32

Query Match 49.1%; Score 27; DB 5; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 3e+05;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEES 6  
 |||||  
 Db 3 CCNTSS 8

## RESULT 6

US-09-089-878-3  
 Sequence 3, Application US/09089878  
 Patent No. 6458528

GENERAL INFORMATION:  
 APPLICANT: Groat, Randall G.  
 APPLICANT: O'Connor, Thomas P.  
 APPLICANT: Mermer, Brian  
 TITLE OF INVENTION: DIAGNOSIS OF FELINE IMMUNODEFICIENCY VIRUS INFECTION  
 TITLE OF INVENTION: USING ENV/GAG POLYPEPTIDE MARKERS  
 FILE REFERENCE: 00088/111001  
 CURRENT APPLICATION NUMBER: US/09/089,878  
 CURRENT FILING DATE: 1998-06-03  
 EARLIER APPLICATION NUMBER: US 60/085,615  
 EARLIER FILING DATE: 1998-05-15  
 NUMBER OF SEQ ID NOS: 3  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 3

## LENGTH: 8

## TYPE: PRT

## ORGANISM: feline immunodeficiency virus

## US-09-089-878-3

Query Match 47.3%; Score 26; DB 4; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 3e+05;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CNEESLIC 9  
 |||||  
 Db 1 CNQNOFFC 8

## RESULT 7

US-09-482-273-199  
 Sequence 199, Application US/09482273  
 Patent No. 6534631

## GENERAL INFORMATION:

APPLICANT: Rosen et al.  
 TITLE OF INVENTION: 71 Human Secreted Proteins  
 FILE REFERENCE: P2030P1  
 CURRENT APPLICATION NUMBER: US/09/482,273  
 CURRENT FILING DATE: 2000-01-13  
 EARLIER APPLICATION NUMBER: PCT/US99/15849  
 EARLIER FILING DATE: 1999-07-14  
 EARLIER APPLICATION NUMBER: 60/092,921  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,922  
 EARLIER FILING DATE: 1998-07-15  
 EARLIER APPLICATION NUMBER: 60/092,956  
 EARLIER FILING DATE: 1998-07-15  
 NUMBER OF SEQ ID NOS: 267  
 SOFTWARE: Patent In Ver. 2.0  
 SEQ ID NO 199  
 LENGTH: 8  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-482-273-199

Query Match 47.3%; Score 26; DB 4; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 3e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNE 4

Db 1 CCNQ 4

## RESULT 8

US-09-258-754-13  
; Sequence 13, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-13

Query Match 47.3%; Score 26; DB 3; Length 9;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CLAKENVVC 9

## RESULT 9

US-09-139-802-93  
; Sequence 93, Application US/09139802  
; Patent No. 6180084  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: P-LJ 3203  
; CURRENT APPLICATION NUMBER: US/09/139,802  
; CURRENT FILING DATE: 1998-08-25  
; EARLIER APPLICATION NUMBER: 08/926,914  
; EARLIER FILING DATE: 1997-09-10  
; EARLIER APPLICATION NUMBER: 08/710,067  
; EARLIER FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-139-802-93

Query Match 47.3%; Score 26; DB 3; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CPEHRSIVC 9

## RESULT 10

US-09-042-107-13  
; Sequence 13, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-13

Query Match 47.3%; Score 26; DB 3; Length 9;  
Best Local Similarity 33.3%; Pred. No. 3e+05;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CLAKENVVC 9

## RESULT 11

US-09-659-786-93  
; Sequence 93, Application US/09659786  
; Patent No. 6491894  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing  
; TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using  
; TITLE OF INVENTION: Same  
; FILE REFERENCE: P-LJ 3203  
; CURRENT APPLICATION NUMBER: US/09/659,786  
; CURRENT FILING DATE: 2000-09-11  
; PRIOR APPLICATION NUMBER: 08/926,914  
; PRIOR FILING DATE: 1997-09-10  
; PRIOR APPLICATION NUMBER: 08/710,067  
; PRIOR FILING DATE: 1996-09-10  
; NUMBER OF SEQ ID NOS: 226  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 93  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-659-786-93

Query Match 47.3%; Score 26; DB 4; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9

Db 1 CPEHRSIVC 9

## RESULT 12

US-08-926-914-93  
; Sequence 93, Application US/08926914



Patent No. 6576239  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Tumor Homing Molecules, Conjugates  
; TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same  
; NUMBER OF SEQUENCES: 199  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: United States  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION NUMBER: US/08/926,914  
; FILING DATE: 10-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2725  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 93:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
; MOLECULE TYPE: peptide  
US-08-926-914-93

Query Match 47.3%; Score 26; DB 4; Length 9;  
Best Local Similarity 44.4%; Pred. No. 3e+05;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCNEESLIC 9  
Db 1 CPEHRSLVC 9

RESULT 13  
US-09-722-250D-13  
; Sequence 13, Application US/09722250D  
; Patent No. 6610651  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 4514  
; CURRENT APPLICATION NUMBER: US/09/722,250D  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-722-250D-13  
Query Match 47.3%; Score 26; DB 4; Length 9;  
Best Local Similarity 33.3%; Pred. No. 3e+05;

Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CCNEESLIC 9  
Db 1 CLAKENVVC 9  
RESULT 14  
US-08-107-411-7  
; Sequence 7, Application US/08107411  
; Patent No. 5340726  
; GENERAL INFORMATION:  
; APPLICANT: Waxman, Lloyd  
; APPLICANT: Connolly, Thomas M.  
; APPLICANT: Keller, Paul  
; TITLE OF INVENTION: PROTEIN FOR INHIBITING  
; TITLE OF INVENTION: COLLAGEN-STIMULATED PLATELET AGGREGATION  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Merck & Co., Inc.  
; STREET: P.O. Box 2000  
; CITY: Rahway  
; STATE: N.J.  
; COUNTRY: USA  
; ZIP: 07065  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/107,411  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/07/844,303  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farr, Richard S.  
; REGISTRATION NUMBER: 32,586  
; REFERENCE/DOCKET NUMBER: 18415  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (908) 594-4958  
; TELEFAX: (908) 594-4720  
; TELEX: ( ) 138825  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 8 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-107-411-7

Query Match 45.5%; Score 25; DB 1; Length 8;  
Best Local Similarity 60.0%; Pred. No. 3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCNEE 5  
Db 4 CCDEK 8

RESULT 15  
US-08-397-633A-100  
; Sequence 100, Application US/08397633A  
; Patent No. 5773577  
; GENERAL INFORMATION:  
; APPLICANT: Cappello, Joseph  
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE  
; TITLE OF INVENTION: OF ENZYMIC CROSS-LINKING  
; NUMBER OF SEQUENCES: 105  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94111-4187  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/397,633A  
 FILING DATE:  
 CLASSIFICATION: 530  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Rowland, Bertram I  
 REGISTRATION NUMBER: 20,015  
 REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 100:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 8 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-397-633A-100

Query Match 45.5%; Score 25; DB 1; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 3e+05;  
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
 QY 2 CNEESLIC 9  
 Db 1 CGOSKVIC 8

Search completed: September 5, 2004, 11:07:04  
 Job time : 12 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 11:00:28 ; Search time 11.6667 Seconds  
(without alignments)  
74.205 Million cell updates/sec

Title: US-09-761-636A-10

Perfect score: 50

Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	17	34.0	8	2	G33098
2	16	32.0	9	2	A60356
3	16	32.0	9	2	PT0247
4	15	30.0	5	2	A60521
5	15	30.0	6	2	I65546
6	15	30.0	7	2	PH0932
7	15	30.0	8	2	PH0803
8	14	28.0	5	2	E60274
9	14	28.0	6	2	F41946
10	14	28.0	8	2	A42057
11	14	28.0	8	2	A35180
12	14	28.0	9	2	A60522
13	14	28.0	9	2	B41983
14	14	28.0	9	2	I52974
15	13	26.0	6	2	I49421
16	13	26.0	6	2	S29881
17	13	26.0	7	2	A12016
18	13	26.0	7	2	S42620
19	13	26.0	8	2	S59622
20	13	26.0	8	2	PQ0701
21	13	26.0	9	2	PT0268
22	12	24.0	6	4	A35039
23	12	24.0	7	2	E61491
24	12	24.0	8	2	S71919
25	12	24.0	8	2	S10783
26	12	24.0	9	2	S36366
27	12	24.0	9	2	G58502
28	12	24.0	9	2	S70334
29	11	22.0	4	2	A32039

## ALIGNMENTS

## RESULT 1

G33098

C:Species: Plasmodium falciparum

C:Date: 24-Aug-1990 #sequence\_revision 24-Aug-1990 #text\_change 09-Jun-2000

C:Accession: G33098

R:Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A:Reference number: A33098

A:Accession: G33098

A>Status: Preliminary

A:Molecule type: protein

A:Residues: 1-8 <NIC>

Query Match

Best Local Similarity 34.0%; Score 17; DB 2; Length 8;

Mismatches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8

DB 2 VPLXLV 7

## RESULT 2

A60356

C:Species: Homo sapiens (man)

C:Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 17-Mar-1999

C:Accession: A60356

R:Shiraishi, Y.

Int. J. Cancer 45, 783-787, 1990

A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr

A:Reference number: A60356; MUID:90216080; PMID:2323853

A:Accession: A60356

A:Molecule type: protein

A:Residues: 1-9 <SHI>

C:Keywords: glycoprotein

Query Match

Best Local Similarity 32.0%; Score 16; DB 2; Length 9;

Mismatches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VPLTSV 8

DB 1 IPLKPV 6

## RESULT 3

PT0247

Ig heavy chain CRD3 region (clone 2-106A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

30	11	22.0	4	2	I54357	schwannomin - mous
31	11	22.0	5	2	B22565	R-phycoerythrin al
32	11	22.0	6	2	B34835	dnaA protein - Pse
33	11	22.0	6	2	PT0280	Ig heavy chain CRD
34	11	22.0	7	2	ECMUCR	catch-relaxing pep
35	11	22.0	7	2	I48105	dihydrofolate redu
36	11	22.0	7	2	I48086	DNA topoisomerase
37	11	22.0	7	2	PH1602	Ig H chain V-D-J r
38	11	22.0	8	2	S19288	acylase - Kluyvera
39	11	22.0	8	2	B39745	endoglycosylcerami
40	11	22.0	8	2	S68802	nitrate reductase
41	11	22.0	8	2	S21288	lectin - potato (f
42	11	22.0	8	2	PT0530	T-cell receptor be
43	11	22.0	8	2	I57018	gene Ctrr protein
44	11	22.0	8	2	A42689	major postsynaptic
45	11	22.0	8	4	I54017	granulocyte-colony

C;Accession: PT0247  
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.  
 J. Exp. Med. 173, 335-407, 1991  
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and  
 A;Reference number: PT0222; MUID:91108337; PMID:1899102  
 A;Accession: PT0247  
 A;Molecule type: DNA  
 A;Residues: 1-9 <YAM>  
 A;Experimental source: B lymphocyte  
 C;Keywords: heterotetramer; immunoglobulin

Query Match 32.0%; Score 16; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SVPLTS 7  
 |||  
 Db 2 SAPIDS 7

RESULT 4  
 A60521  
 Glycogen phosphorylase (EC 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
 N;Alternate names: glycogen phosphorylase b  
 C;Species: Liza ramada  
 C;Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 18-Aug-2003  
 C;Accession: A60521  
 R;Bonamusa, L.; Baanante, I.V.  
 Comp. Biochem. Physiol. B 95, 295-301, 1990

A;Title: Purification and characterization of glycogen phosphorylase B from skeletal muscle  
 A;Reference number: A60521; MUID:90227907; PMID:2109669  
 A;Accession: A60521  
 A;Molecule type: protein  
 A;Residues: 1-5 <BON>

C;Superfamily: glucan phosphorylase  
 C;Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
 F;3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experiment

Query Match 30.0%; Score 15; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4  
 |||  
 Db 3 SVP 5

RESULT 5  
 I65546  
 MHC H2-L antigen - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
 C;Accession: I65546  
 R;Kimura, A.; Israel, A.; Le Bail, O.; Kourilsky, P.  
 Cell 44, 261-272, 1986  
 A;Title: Detailed analysis of the mouse H-2Kb promoter: Enhancer-like sequences and the  
 A;Reference number: I52778; MUID:96106202; PMID:3510743  
 A;Accession: I65546  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-6 <RES>  
 A;Cross-references: GB:M12483; NID:g199565; PIDN:AAA39663.1; PID:g554234

Query Match 30.0%; Score 15; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 VPCT 6  
 |||  
 Db 2 VPCT 5

RESULT 6

PH0932  
 T-cell receptor beta chain V-D-J region (clone 3) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0932  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0932  
 A;Molecule type: mRNA  
 A;Residues: 1-7 <GOL>  
 A;Experimental source: complete Freund's adjuvant-immunized lymph node  
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSVP 4  
 |||  
 Db 1 CASP 4

RESULT 7  
 PH0803  
 T-cell receptor alpha chain (J2) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PH0803  
 R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.  
 J. Exp. Med. 174, 1371-1383, 1991  
 A;Title: T cell receptor genes in a series of class I major histocompatibility complex-  
 allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0803  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <CAS>  
 A;Cross-references: EMBL:X60912  
 A;Experimental source: T lymphocyte  
 C;Keywords: T-cell receptor

Query Match 30.0%; Score 15; DB 2; Length 8;  
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CSVPILT 6  
 ||: ||  
 Db 1 CAAGIT 6

RESULT 8  
 E60274  
 major protein antigen MP763 - Mycobacterium tuberculosis (fragment)  
 C;Species: Mycobacterium tuberculosis  
 C;Date: 11-Dec-1992 #sequence\_revision 11-Dec-1992 #text\_change 30-Sep-1993  
 C;Accession: E60274  
 R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
 Infect. Immun. 59, 372-382, 1991  
 A;Title: Isolation and partial characterization of major protein antigens in the culture  
 A;Reference number: A60274; MUID:91099989; PMID:1898899  
 A;Accession: E60274  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-5 <NAG>

Query Match 28.0%; Score 14; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 PLT 6  
 ||: ||  
 Db 3 PIT 5

```

RESULT 9
F41946
T-cell receptor gamma chain (1a.27) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: F41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A:Reference number: A41946; MUID:92049316; PMID:1658619
A:Accession: F41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-6 <WER>
C:Keywords: T-cell receptor

Query Match      28.0%; Score 14; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches      2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 CSV 3
      | |
DB      2 CAV 4

RESULT 10
A42057
fibroblast growth factor receptor 1, secreted - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42057
R:Werner, S.; Duan, D.S.R.; de Vries, C.; Peters, K.G.; Johnson, D.E.; Williams, L.T.
Mol. Cell. Biol. 12, 82-88, 1992
A:Title: Differential splicing in the extracellular region of fibroblast growth factor r
A:Reference number: A42057; MUID:92107200; PMID:1309595
A:Accession: A42057
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <WER>
A:Cross-references: GB:M80363
C:Keywords: growth factor receptor

Query Match      28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches      4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 VPLTS 7
      | | |
DB      1 VLLTS 5

RESULT 11
A35180
neutral proteinase (EC 3.4.-.-), calcium-activated - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 21-Mar-1996
C:Accession: A35180
R:Yoshinara, Y.; Ueda, H.; Fujii, N.; Shide, A.; Yajima, H.; Satoh, M.
J. Biol. Chem. 265, 5809-5815, 1990
A:Title: Purification of a novel type of calcium-activated neutral protease from rat bra
A:Reference number: A35180; MUID:90202830; PMID:2319836
A:Accession: A35180
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <YOS>
C:Keywords: hydrolase

Query Match      28.0%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches      3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      4 PLTS 7
      | |
DB      1 PLLS 4

RESULT 12
A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60522
R:Yoshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Suzuki
Comp. Biochem. Physiol. B 95, 423-429, 1990
A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea urchi
A:Reference number: A60522; MUID:90227916; PMID:2158412
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <YOS>
C:Superfamily: unassigned animal peptides
F:2-9/Disulfide bonds: #status experimental

Query Match      28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches      2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      7 SVC 9
      | |
DB      7 AVC 9

RESULT 13
B41983
orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
C:Species: Azotobacter vinelandii
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: B41983
R:Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
A:Title: Unification of the ferritin family of proteins.
A:Reference number: A41983; MUID:92196129; PMID:1549605
A:Accession: B41983
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid; protein
A:Residues: 1-9 <GRO>
A:Cross-references: GB:M83692; NID:gl42297; PIDN:AAA22122.1; PID:gl42299
A:Note: sequence extracted from NCHI backbone (NCBIP:88442)

Query Match      28.0%; Score 14; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches      3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 PLTS 7
      | |
DB      4 PRTS 7

RESULT 14
I52974
seminal vesicle protein IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I52974
R:Yang, C.T.; Harris, S.B.
DNA 2, 105-111, 1983
A:Title: The seminal vesicle secretion IV gene: detection of S1 nuclease-sensitive sites
A:Reference number: I52974; MUID:83261204; PMID:6307619
A:Accession: I52974
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <RES>
A:Cross-references: GB:M27324; NID:g207124; PIDN:AAA63501.1; PID:g207125
C:Genetics:
A:Gene: SVSIV

```

Query Match 28.0%; Score 14; DB 2; Length 9;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTSV 8  
| | | |  
Db 3 LTSL 6

## RESULT 15

I49421  
laminin B1 - western wild mouse (fragment)  
C:Species: Mus spretus (western wild mouse)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
C:Accession: I49421  
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, J.H.  
Mamm. Genome 5, 349-355, 1994  
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.  
A:Reference number: I49334; MUID:94319082; PMID:8043949  
A:Accession: I49421  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-6 <RES>  
A:Cross-references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829

Query Match 26.0%; Score 13; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SVC 9  
| | |  
Db 3 STC 5

Search completed: September 5, 2004, 11:06:22  
Job time : 11.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 5, 2004, 10:57:02 ; Search time 7 Seconds  
(without alignments)  
66.947 Million cell updates/sec

Title: US-09-761-636A-10  
Perfect score: 50  
Sequence: 1 CSVPLTSVC 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 251

Minimum DB seq length: 0  
Maximum DB seq length: 9

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	19	38.0	9	1 MGMT_BOVIN	P29177 bos taurus
2	14	28.0	8	1 ACT_CARMA	P80709 carcinus ma
3	14	28.0	9	1 YBFR_AZOVI	P25825 azotobacter
4	13	26.0	6	1 E101_LITRU	P82096 litorea rub
5	12	24.0	8	1 AL16_CVPCO	P84157 cydia pomon
6	12	24.0	8	1 FUSF_FUSCO	P81010 fusarium so
7	12	24.0	8	1 UPAL_HUMAN	P30087 homo sapien
8	12	24.0	9	1 FAR5_PENMO	P83320 penaeus mon
9	12	24.0	9	1 FLA2_TREHY	P80159 treponema h
10	12	24.0	9	1 OXYA_SCYCA	P42996 scyliorhinu
11	12	24.0	9	1 OXYF_SCYCA	P42997 scyliorhinu
12	12	24.0	9	1 OXYT_BUFRE	P42995 bufo regula
13	12	24.0	9	1 OXYV_SQUAC	P43000 squalus aca
14	11	22.0	6	1 VP19_HSVIK	P23210 herpes simp
15	11	22.0	7	1 CARP_MYTED	P10420 mytilus edu
16	11	22.0	7	1 MNP1_LEPDE	P42984 leptinotars
17	11	22.0	7	1 TPYV_PACDA	P83455 pachymedusa
18	11	22.0	8	1 PPK3_PERAM	P84618 periplaneta
19	11	22.0	8	1 VGIG_HSV2B	P81780 herpes simp
20	11	22.0	9	1 COXE_THUOB	P80975 thunnus obe
21	11	22.0	9	1 FAR9_ASCSU	P43172 ascaris suu
22	11	22.0	9	1 ISOT_CVPCA	P42993 cyprinus ca
23	11	22.0	9	1 LMT3_LOCMI	P41489 locusta mig
24	11	22.0	9	1 OXYA_SQUAC	P42999 squalus aca
25	11	22.0	9	1 OXYT_EISFO	P42998 eisenia foe
26	11	22.0	9	1 OXYT_OCTVU	P80027 octopus vul
27	11	22.0	9	1 OXYT_RABIT	P32878 oryctolagus
28	11	22.0	9	1 RT33_BOVIN	P82926 bos taurus
29	11	22.0	9	1 TAL3_PICJA	P17441 pichia jadi
30	11	22.0	9	1 UP43_HUMAN	P30089 homo sapien
31	11	22.0	9	1 UP47_HUMAN	P30093 homo sapien
32	10	20.0	7	1 TY51_LITRU	P82065 litorea rub
33	10	20.0	8	1 UPAA_HUMAN	P30096 homo sapien

34 10 20.0 9 1 CCAP\_CARMA P38556 carcinus ma  
35 10 20.0 9 1 CONO\_CONGE P05486 conus geogr  
36 10 20.0 9 1 CONO\_CONST P05487 conus stria  
37 10 20.0 9 1 DNFI\_LOCMI P16339 locusta mig  
38 10 20.0 9 1 OXYT\_CVPCA P23879 cyprinus ca  
39 10 20.0 9 1 OXYT\_RAJCL P42994 raja clavav  
40 10 20.0 9 1 PPK1\_PERAM P82691 periplaneta  
41 10 20.0 9 1 TAL1\_PICJA P17440 pichia jadi  
42 9 18.0 5 1 E103\_LITRU P82099 litorea rub  
43 9 18.0 6 1 CIP1\_MYTED P13736 mytilus edu  
44 9 18.0 6 1 CIP2\_MYTED P13737 mytilus edu  
45 9 18.0 7 1 BRHP\_CONIM P58603 conus imper

## ALIGNMENTS

RESULT 1  
MGMT\_BOVIN  
ID\_MGMT\_BOVIN STANDARD; PRT; 9 AA.  
AC P29177;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-DEC-1992 (Rel. 24, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (Fragment).  
DE methylguanine-DNA methyltransferase (Fragment).  
GN MGMT.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Thymus;  
RX MEDLINE=90174912; PubMed=2308822;  
RA Rydberg B., Hall J., Karan P.;  
RT "Active site amino acid sequence of the bovine O6-methylguanine-DNA methyltransferase.";  
RL Nucleic Acids Res. 18:17-21(1990).  
CC -!- FUNCTION: Repair of alkylated guanine in DNA by stoichiometrically transferring the alkyl group at the O-6 position to a cysteine residue in the enzyme. This is a suicide reaction: the enzyme is irreversibly inactivated.  
CC -!- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) + protein [protein]-L-cysteine = DNA (without 6-O-methylguanine) + protein S-methyl-L-cysteine.  
CC -!- SIMILARITY: WITH SEGMENTS OF E.COLI ADA AND OGT METHYLTRANSFERASE WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.  
DR InterPro: IPR001497; Methyltransf\_1.  
DR PROSITE: PS00374; MGMT; PARTIAL.  
KW DNA repair; transferase; Methyltransferase.  
FT NON\_TER 1  
FT ACT\_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).  
FT NON\_TER 9 9  
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 38.0%; Score 19; DB 1; Length 9;  
Best Local Similarity 28.6%; Pred. No. 1.4e+05;  
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 3 VPLTSVC 9  
Db 3 IPILTPC 9

RESULT 2  
ACT\_CARMA  
ID\_ACT\_CARMA STANDARD; PRT; 8 AA.  
AC P80709;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Actin (Fragment).  
 OS Carcinus maenas (Common shore crab) (Green crab).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RA Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,  
 RA Baghdassarian D.;  
 RT "A transaldolase. An enzyme implicated in crab steroidogenesis.";  
 RL Endocrine 5:23-32(1996).  
 CC -1- FUNCTION: Actins are highly conserved proteins that are involved  
 CC in various types of cell motility and are ubiquitously expressed  
 CC in all eukaryotic cells.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:  
 CC 6.8, ITS MW IS: 46 kDa.  
 CC -1- SIMILARITY: Belongs to the actin family.  
 DR InterPro; IPR004001; Actin.  
 DR InterPro; IPR004000; Actin-like.  
 DR PROSITE; PS00406; ACTINS\_1; PARTIAL.  
 DR PROSITE; PS00432; ACTINS\_2; PARTIAL.  
 DR PROSITE; PS01132; ACTINS\_ACT\_LIKE; PARTIAL.  
 KW Structural protein.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 SQ SEQUENCE 8 AA; 976 MW; 1424005AB2CAAE3 CRC64;  
 Query Match 28.0%; Score 14; DB 1; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 CSVPVL 5  
 DB 2 CDVDI 6  
 RESULT 3  
 YBFR\_AZOVI  
 ID YBFR\_AZOVI STANDARD; PRT; 9 AA.  
 AC P25825;  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein in bfr 3' region (Fragment).  
 OS Azotobacter vinelandii.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Azotobacter.  
 OX NCBI\_TaxID=354;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92196129; PubMed=1549605;  
 RA Grossman M.J., Hinton S.M., Minak-Bernero V., Slaughter C.,  
 RA Stiefel E.I.;  
 RT "Unification of the ferritin family of proteins.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2419-2423(1992).  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 -----  
 DR EMBL; M83692; AAA22122.1; .  
 DR PIR; B41983; B41983.  
 KW Hypothetical protein.  
 FT NON\_TER 9 9  
 SQ SEQUENCE 9 AA; 947 MW; DF98B5A1B41776D CRC64;  
 Query Match 28.0%; Score 14; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4 PLTS 7  
 DB 4 PRTS 7  
 RESULT 4  
 EI01\_LITRU  
 ID EI01\_LITRU STANDARD; PRT; 6 AA.  
 AC P82096;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Electrin 1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RT "Peptides from the skin glands of the Australian buzzing tree frog  
 RT Litoria electrica. Comparison with the skin peptides from Litoria  
 RT rubella";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KW Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5 6  
 FT MOD\_RES 6 6  
 SQ SEQUENCE 6 AA; 792 MW; 5683704772C9A000 CRC64;  
 Query Match 26.0%; Score 13; DB 1; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 VPL 5  
 DB 2 VPI 4  
 RESULT 5  
 ALL6\_CYDPO  
 ID ALL6\_CYDPO STANDARD; PRT; 8 AA.  
 AC P82157;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Cydiastatin 6.  
 OS Cydia pomonella (Codling moth).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;  
 OC Tortricidae; Tortricidae; Olethreutinae; Cydia.  
 OX NCBI\_TaxID=82600;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Larva;  
 RX MEDLINE=98054539; PubMed=9392829;  
 RA Dave H., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,  
 RA Davey M., East P.D., Thorpe A.;  
 RT "Lepidopteran peptides of the allatostatin superfamily.";  
 RL Peptides 18:1301-1309(1997).  
 CC -1- SIMILARITY: Belongs to the allatostatin family.  
 KW Neuropeptide; Amidation.  
 FT MOD\_RES 8 8  
 FT MOD\_RES 8 8  
 SQ SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;  
 Query Match 24.0%; Score 12; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;



QY 3 VPL 5  
Db 1 LPL 3

## RESULT 6

FUSS\_FUSSO  
ID\_FUSS\_FUSSO STANDARD; PRT; 8 AA.  
AC P81010;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Allergen Fus s 13596\* (Fragment).  
OS Fusarium solani (subsp. pisi) (Nectria haematococca).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.  
OX NCBI\_TaxID=70791;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=IARI 3596; TISSUE=Mycelium;  
RA Verma J.; Gangal S.V.;  
RL Submitted (JUL-1997) to Swiss-Prot.  
CC -!- ALLERGEN: Causes an allergic reaction in human.  
KW Allergen.  
FT NON TER 8  
SQ SEQUENCE 8 AA; 898 MW; C372C441F5B69041 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4  
Db 6 NVP 8

## RESULT 7

UPAL\_HUMAN  
ID\_UPAL\_HUMAN STANDARD; PRT; 8 AA.  
AC P30087;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Unknown protein from 2D-page of plasma (Spot 2) (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Plasma;  
RA MEDLINE=93092937; PubMed=1459097;  
RX Hughes G.J.; Frutiger S.; Paquet N.; Ravier F.; Pasquali C.;  
RA Sanchez J.-C.; James R.; Tissot J.-D.; Bjellqvist B.;  
RA Hochstrasser D.F.;  
RT "Plasma protein map: an update by microsequencing."  
RL Electrophoresis 13:707-714(1992).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.9, its MW is: 65 kDa.  
DR SWISS-2DPAGE; P30087; HUMAN.  
FT NON TER 1  
FT NON TER 8  
FT NON TER 8  
SQ SEQUENCE 8 AA; 944 MW; C01772C455BB06DA CRC64;

Query Match 24.0%; Score 12; DB 1; Length 8;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4  
Db 5 NVP 7

## RESULT 8

FARS\_PENMO  
ID\_FARS\_PENMO STANDARD; PRT; 9 AA.  
AC P83320;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE FMRamide-like neuropeptide FLPS (SMPSRLRF-amide).  
OC Penaeus monodon (Penaeid shrimp).  
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;  
OC Penaeidae; Penaeus.  
OX NCBI\_TaxID=6687;  
RN [1]  
RP SEQUENCE, AND MASS SPECTROMETRY.  
RC TISSUE=Eyestalk;  
RX MEDLINE=21956277; PubMed=11959015;  
RA Sithigorngul P.; Pupum J.; Krungkasem C.; Longyant S.;  
RA Chaivuthangkura P.; Sithigorngul W.; Petsom A.;  
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk of the giant tiger prawn Penaeus monodon."  
RL Comp. Biochem. Physiol. 131B:325-337(2002).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- MASS SPECTROMETRY: MW=1121.1; METHOD=MALDI.  
CC -!- SIMILARITY: Belongs to the FARP (FMRamide related peptide) family.  
DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.  
KW Neuropeptide; Amidation.  
FT MOD RES 9  
SQ SEQUENCE 9 AA; 1106 MW; B60B07340735A766 CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;  
Best Local Similarity 66.7%; Pred. No. 1.4e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4  
Db 1 SMP 3

## RESULT 9

FLA2\_TREHY  
ID\_FLA2\_TREHY STANDARD; PRT; 9 AA.  
AC P80159;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Flagellar filament outer layer protein flaA2 (35 kDa sheath protein) (Fragment).  
GN FLA2.  
OC Treponema hyodysenteriae (Serpulina hyodysenteriae).  
OC Bacteria; Spirochaetes; Spirochaetales; Brachyspiraceae; Brachyspira.  
OX NCBI\_TaxID=159;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=CS;  
RX MEDLINE=93139764; PubMed=1487733;  
RA Koopman M.B.H.; Baats E.; van Vorstenbosch C.J.A.H.V.;  
RA van der Zeijst B.A.M.; Kusters J.G.;  
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are composed of two sheath proteins and three core proteins."  
RL J. Gen. Microbiol. 138:2697-2706(1992).  
CC -!- FUNCTION: Component of the outer layer of the flagella.  
CC -!- SUBUNIT: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO SHEATH PROTEINS, FLA1 (44 kDa) AND FLA2 (35 kDa) AROUND A CORE THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND FLAB3 (32 kDa).  
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.  
KW Flagellum; Periplasmic.  
FT UNSURE 2  
FT UNSURE 8  
FT UNSURE 9

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FT NON TER          9          9      855A19C68B4772D1 CRC64;
SQ SEQUENCE 9 AA; 1129 MW; 24.0%; Score 12; DB 1; Length 9;
Query Match
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVP 4
Db 2 TVP 4

RESULT 10
OXYA_SCYCA
ID OXYA_SCYCA STANDARD; PRT; 9 AA.
AC P42996;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Asvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
RN [1]
RP SEQUENCE
RC TISSUE=Pituitary; PubMed=7972045;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone, Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

RESULT 11
OXYF_SCYCA
ID OXYF_SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
NCBI_TaxID=7830;
RN [1]
RP SEQUENCE
RC TISSUE=Pituitary; PubMed=7972045;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone, Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 982 MW; 17EDD76EB44404B CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

RESULT 12
OXYT_BUPRE
ID OXYT_BUPRE STANDARD; PRT; 9 AA.
AC P42995;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Seritocin (Iser5,Ile8]-oxytocin).
OS Bufo regularis (Leopard toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Bufonidae; Bufo.
NCBI_TaxID=8390;
RN [1]
RP SEQUENCE
RC TISSUE=Pituitary neurointermediate lobe;
RX MEDLINE=96059313; PubMed=7591488;
RA Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.;
RT "A new neurohypophysial peptide, seritocin (Iser5,Ile8]-oxytocin),
RT identified in a dryness-resistant African toad, Bufo regularis.";
RL Int. J. Pept. Protein Res. 45:482-487(1995).
CC -!- FUNCTION: Devoid of oxytocic activity.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
KW Hormone, Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 983 MW; 17FF476EA5A6D04B CRC64;

Query Match
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SVPL 5
Db 5 SCPI 8

RESULT 13
OXYV_SQUAC
ID OXYV_SQUAC STANDARD; PRT; 9 AA.
AC P43000;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Valitocin.
OS Squalus acanthias (Spiny dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Squaloidei; Squalidae; Squalus.
NCBI_TaxID=7797;

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RT isolated from the spotted dogfish (Scyliorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone, Amidation.
FT DISULFID 1 6
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
Db 6 CPV 8

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[1]
RN RP SEQUENCE.
RX MEDLINE=73031727; PubMed=5083097;
RA Acher R., Chauvet J., Chauvet M.-T.;
RT "Phylogeny of the neurohypophysial hormones. Two new active peptides
RL isolated from a cartilaginous fish, Squalus acanthias.";
RL Eur. J. Biochem. 29:12-19(1972).
[2]
RN RP SEQUENCE.
RX MEDLINE=72128038; PubMed=4622083;
RA Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
RT "Identification of 2 new neurohypophyseal hormones, valitocin (Val8-
RT oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the
RT spiny dog-fish (Squalus acanthias).";
RL C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000381; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 996 MW; 17EDD76EB456D04B CRC64;

Query Match 24.0%; Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CSV 3
DB | |
6 CPV 8

RESULT 14
VP19_HSV1K
ID VP19_HSV1K STANDARD; PRT; 6 AA.
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -!- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -!- SIMILARITY: Belongs to the herpesviruses VP19C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M57646; AAA45830.1; -
KW Capsid assembly; Coat protein; DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 6;
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Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PL 5
DB | |
5 PL 6

RESULT 15
CARP MYTED
ID CARP MYTED STANDARD; PRT; 7 AA.
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]_TaxID=6550;
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia.";
RL Brain Res. 422:374-376(1987).
CC -!- FUNCTION: This peptide exhibits both potentiating (contraction)
CC and inhibitory (relaxation) effects on the anterior byssus
CC retractor muscle.
DR PIR; A29342; BCMUCR.
KW Hormone; Amidation.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 22.0%; Score 11; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.4e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 SVPL 5
DB | |
1 AMPM 4

Search completed: September 5, 2004, 11:04:00
Job time : 7 secs
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